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(54) Title: OSTEOINDUCTIVE COMPOSITIONS

(57) Abstract

Purified BMP-5, BMP-6 and BMP-7 proteins and processes for producing them are disclosed. The proteins may be used in the treatment of bone and/or cartilage defects and in wound healing and related tissue repair.

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OSTEOINDUCTIVE COMPOSITIONS

The present invention relates to proteins having utility in the formation of bone and/or cartilage. In particular the invention relates to a number of families of purified proteins, termed BMP-5, BMP-6 and BMP-7 protein families (wherein BMP is Bone Morphogenic Protein) and processes for obtaining them. These proteins may exhibit the ability to induce cartilage and/or bone formation. They may be used to induce bone and/or cartilage formation and in wound healing and tissue repair.

The invention provides a family of BMP-5 proteins. Purified human BMP-5 proteins are substantially free from other proteins with which they are co-produced, and characterized by an amino acid sequence comprising from amino acid #323 to amino acid #454 set forth in Table III. This amino acid sequence #323 to #454 is encoded by the DNA sequence comprising nucleotide #1665 to nucleotide #2060 of Table III. BMP-5 proteins may be further characterized by an apparent molecular weight of 28,000-30,000 daltons as determined by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). Under reducing conditions in SDS-PAGE the protein electrophoreses with a molecular weight of approximately 14,000 - 20,000 daltons. It is contemplated that these proteins are capable of stimulating, promoting, or otherwise inducing cartilage and/or bone formation.

The invention further provides bovine BMP-5 proteins comprising amino acid #9 to amino acid #140 set forth in Table I. The amino acid sequence

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from #9 to #140 is encoded by the DNA sequence comprising nucleotide #32 to #427 of Table I. These proteins may be further characterized by an apparent molecular weight of 28,000 - 30,000 daltons as determined by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). Under reducing conditions in SDS-PAGE the protein electrophoreses with a molecular weight of approximately 14,000-20,000 daltons. It is contemplated that these proteins are capable of inducing cartilage and/or bone formation.

Human BMP-5 proteins of the invention may be produced by culturing a cell transformed with a DNA sequence containing the nucleotide sequence the same or substantially the same as the nucleotide sequence shown in Table III comprising nucleotide #699 to nucleotide #2060. BMP-5 proteins comprising the amino acid sequence the same or substantially the same as shown in Table III from amino acid # 323 to amino acid # 454 are recovered, isolated and purified from the culture medium.

Bovine BMP-5 proteins may be produced by culturing a cell transformed with a DNA sequence containing the nucleotide sequence the same or substantially the same as that shown in Table I comprising nucleotide #8 through nucleotide #427 and recovering and purifying from the culture medium a protein containing the amino acid sequence or a portion thereof as shown in Table I comprising amino acid #9 to amino acid #140.

The invention provides a family of BMP-6 proteins. Purified human BMP-6 proteins, substantially free from other proteins with which they are co-produced and are characterized by an amino acid sequence comprising acid #382 to amino

acid #513 set forth in Table IV. The amino acid sequence from amino acid #382 to #513 is encoded by the DNA sequence of Table IV from nucleotide #1303 to nucleotide #1698. These proteins may be further characterized by an apparent molecular weight of 28,000-30,000 daltons as determined by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). Under reducing conditions in SDS-PAGE the protein electrophoreses with a molecular weight of approximately 14,000 - 20,000 daltons. It is contemplated that these proteins are capable of stimulating promoting, or otherwise inducing cartilage and/or bone formation.

The invention further provides bovine BMP-6 proteins characterized by the amino acid sequence comprising amino acid #121 to amino acid #222 set forth in Table II. The amino acid sequence from #121 to #222 is encoded by the DNA sequence of Table II from nucleotide #361 to #666 of Table II. These proteins may be further characterized by an apparent molecular weight of 28,000 - 30,000 daltons as determined by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). Under reducing conditions in SDS-PAGE the protein electrophoreses with a molecular weight of approximately 14,000-20,000 daltons. It is contemplated that these proteins are capable of inducing cartilage and/or bone formation.

Human BMP-6 proteins of the invention are produced by culturing a cell transformed with a DNA sequence comprising nucleotide #160 to nucleotide #1698 as shown in Table III or a substantially similar sequence. BMP-6 proteins comprising amino acid #382 to amino acid #513 or a substantially similar sequence are recovered, isolated and

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purified from the culture medium.

Bovine BMP-6 proteins may be produced by culturing a cell transformed with a DNA comprising nucleotide #361 through nucleotide #666 as set forth in Table II or a substantially similar sequence and recovering and purifying from the culture medium a protein comprising amino acid #121 to amino acid #222 as set forth in Table II.

The invention provides a family of BMP-7 proteins. Which includes purified human BMP-7 proteins, substantially free from other proteins with which they are co-produced. Human BMP-7 proteins are characterized by an amino acid sequence comprising amino acid #300 to amino acid #431 set forth in Table V. This amino acid sequence #300 to #431 is encoded by the DNA sequence of Table V from nucleotide #994 to #1389. BMP-7 proteins may be further characterized by an apparent molecular weight of 28,000-30,000 daltons as determined by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). Under reducing conditions in SDS-PAGE the protein electrophoreses with a molecular weight of approximately 14,000 - 20,000 daltons. It is contemplated that these proteins are capable of stimulating, promoting, or otherwise inducing cartilage and/or bone formation.

Human BMP-7 proteins of the invention may be produced by culturing a cell transformed with a DNA sequence containing the nucleotide sequence the same or substantially the same as the nucleotide sequence shown in Table V comprising nucleotide # 97 to nucleotide #1389. BMP-7 proteins comprising the amino acid sequence the same or substantially the same as shown in Table V from amino acid #300

to amino acid #431 are recovered, isolated and purified from the culture medium.

The invention further provides a method wherein the proteins described above are utilized for obtaining related human protein/s or other mammalian cartilage and/or bone formation protein/s. Such methods are known to those skilled in the art of genetic engineering. One method for obtaining such proteins involves utilizing the human BMP-5, BMP-6 and BMP-7 coding sequences or portions thereof to design probes for screening human genomic and/or cDNA libraries to isolate human genomic and/or cDNA sequences. Additional methods within the art may employ the bovine and human BMP proteins of the invention to obtain other mammalian BMP cartilage and/or bone formation proteins.

Having identified the nucleotide sequences, the proteins are produced by culturing a cell transformed with the nucleotide sequence. This sequence or portions thereof hybridizes under stringent conditions to the nucleotide sequence of either BMP-5, BMP-6 or BMP-7 proteins and encodes a protein exhibiting cartilage and/or bone formation activity. The expressed protein is recovered and purified from the culture medium. The purified BMP proteins are substantially free from other proteinaceous materials with which they are co-produced, as well as from other contaminants.

BMP-5, BMP-6 and BMP-7 proteins may be characterized by the ability to promote, stimulate or otherwise induce the formation of cartilage and/or bone formation. It is further contemplated that the ability of these proteins to induce the

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formation of cartilage and/or bone may be exhibited by the ability to demonstrate cartilage and/or bone formation activity in the rat bone formation assay described below. It is further contemplated that the proteins of the invention demonstrate activity in this rat bone formation assay at a concentration of 10 μ g - 500 μ g/gram of bone formed. More particularly, it is contemplated these proteins may be characterized by the ability of 1 μ g of the protein to score at least +2 in the rat bone formation assay described below using either the original or modified scoring method.

Another aspect of the invention provides pharmaceutical compositions containing a therapeutically effective amount of a BMP-5, BMP-6 or BMP-7 protein in a pharmaceutically acceptable vehicle or carrier. Further compositions comprise at least one BMP-5, BMP-6 or BMP-7 protein. It is therefore contemplated that the compositions may contain more than one of the BMP proteins of the present invention as BMP-5, BMP-6 and BMP-7 proteins may act in concert with or perhaps synergistically with one another. The compositions of the invention are used to induce bone and/or cartilage formation. These compositions may also be used for wound healing and tissue repair.

Further compositions of the invention may include in addition to a BMP-5, BMP-6 or BMP-7 protein of the present invention at least one other therapeutically useful agent such as the proteins designated BMP-1, BMP-2 (also having been designated in the past as BMP-2A, BMP-2 Class I), BMP-3 and BMP-4 (also having been designated in the past as BMP-2B and BMP-2 Class II) disclosed in co-owned International Publication WO88/00205

published 14 January 1988 and International Publication WO89/10409 published 2 November 1989. Other therapeutically useful agents include growth factors such as epidermal growth factor (EGF),
5 fibroblast growth factor (FGF), transforming growth factors (TGF- α and TGF- β), and platelet derived growth factor (PDGF).

The compositions of the invention may also include an appropriate matrix, for instance, for
10 delivery and/or support of the composition and/or providing a surface for bone and/or cartilage formation. The matrix may provide slow release of the BMP protein and/or the appropriate environment for presentation of the BMP protein of the
15 invention.

The compositions of the invention may be employed in methods for treating a number of bone and/or cartilage defects, and periodontal disease. They may also be employed in methods for treating
20 various types of wounds and in tissue repair. These methods, according to the invention, entail administering a composition of the invention to a patient needing such bone and/or cartilage formation, wound healing or tissue repair. The
25 method therefore involves administration of a therapeutically effective amount of a protein of the invention. These methods may also entail the administration of a protein of the invention in conjunction with at least one of the "BMP" proteins
30 disclosed in the co-owned applications described above. In addition, these methods may also include the administration of a protein of the invention with other growth factors including EGF, FGF, TGF- α , TGF- β , and PDGF.

35 Still a further aspect of the invention are

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DNA sequences coding for expression of a protein of the invention. Such sequences include the sequence of nucleotides in a 5' to 3' direction illustrated in Tables I - V or DNA sequences which hybridize under stringent conditions with the DNA sequences of Tables I - V and encode a protein demonstrating ability to induce cartilage and/or bone formation. Such cartilage and/or bone formation may be demonstrated in the rat bone formation assay described below. It is contemplated that these proteins may demonstrate activity in this assay at a concentration of 10 μ g - 500 μ g/gram of bone formed. More particularly, it is contemplated that these proteins demonstrate the ability of 1 μ g of the protein to score at least +2 in the rat bone formation assay. Finally, allelic or other variations of the sequences of Tables I - V whether such nucleotide changes result in changes in the peptide sequence or not, are also included in the present invention.

A further aspect of the invention provides vectors containing a DNA sequence as described above in operative association with an expression control sequence therefor. These vectors may be employed in a novel process for producing a protein of the invention in which a cell line transformed with a DNA sequence directing expression of a protein of the invention in operative association with an expression control sequence therefor, is cultured in a suitable culture medium and a protein of the invention is recovered and purified therefrom. This claimed process may employ a number of known cells, both prokaryotic and eukaryotic, as host cells for expression of the polypeptide. The recovered BMP proteins are

purified by isolating them from other proteinaceous materials with which they are co-produced as well as from other contaminants.

Other aspects and advantages of the present invention will be apparent upon consideration of the following detailed description and preferred embodiments thereof.

Detailed Description of the Invention

Purified human BMP-5 proteins may be produced by culturing a host cell transformed with the DNA sequence of Table III. The expressed BMP-5 proteins are isolated and purified from the culture medium. Purified human BMP-5 proteins are expected to be characterized an amino acid sequence comprising amino acid #323 to #454 as shown in Table III. Purified BMP-5 human cartilage/bone proteins of the present invention are therefore produced by culturing a host cell transformed with a DNA sequence comprising nucleotide #699 to nucleotide #2060 as shown in Table III or substantially homologous sequences operatively linked to a heterologous regulatory control sequence and recovering and purifying from the culture medium a protein comprising the amino acid sequence as shown in Table III from amino acid #323 to amino acid #454 or a substantially homologous sequence.

In further embodiments the DNA sequence comprises the nucleotides encoding amino acids #323-#454. BMP-5 proteins may therefore be produced by culturing a host cell transformed with a DNA sequence comprising nucleotide #1665 to nucleotide #2060 as shown in Table III or substantially homologous sequences operatively linked to a

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heterologous regulatory control sequence and recovering and purifying from the culture medium a protein comprising amino acid #323 to amino acid #454 as shown in Table III or a substantially homologous sequence. The purified human BMP-5 proteins are substantially free from other proteinaceous materials with which they are co-produced, as well as from other contaminants.

Purified BMP-5 bovine cartilage/bone proteins of the present invention are produced by culturing a host cell transformed with a DNA sequence comprising the DNA sequence as shown in Table I from nucleotide # 8 to nucleotide # 578 or substantially homologous sequences and recovering and purifying from the culture medium a protein comprising the amino acid sequence as shown in Table I from amino acid # 9 to amino acid # 140 or a substantially homologous sequence. The purified BMP-5 bovine proteins as well as all of the BMP proteins of the invention, are substantially free from other proteinaceous materials with which they are co-produced, as well as from other contaminants.

Purified human BMP-6 proteins may be produced by culturing a host cell transformed with the DNA sequence of Table IV. The expressed proteins are isolated and purified from the culture medium. Purified human BMP-6 proteins of the invention are expected to be characterized by an amino acid sequence comprising amino acid #382 to #513 as set forth in Table IV. These purified BMP-6 human cartilage/bone proteins of the present invention are therefore produced by culturing a host cell transformed with a DNA sequence comprising nucleotide #160 to nucleotide #1698 as set forth

in Table IV or substantially homologous sequence
operatively linked to a heterologous regulatory
control sequence and recovering, isolating and
purifying from the culture medium a protein
5 comprising amino acid #382 to amino acid #513 as
set forth in Table IV or a substantially homologous
sequence.

Further embodiments may utilize the DNA
sequence comprising the nucleotides encoding amino
10 acids #382 - #513. Purified human BMP-6 proteins
may therefore be produced by culturing a host cell
transformed with the DNA sequence comprising
nucleotide #1303 to #1698 as set forth in Table IV
or substantially homologous sequences operatively
15 linked to a heterologous regulatory control
sequence and recovering and purifying from the
culture medium a protein comprising amino acid #382
to #513 as set forth in Table IV or a substantially
homologous sequence. The purified human BMP-6
20 proteins are substantially free from other
proteinaceous materials with which they are co-
produced, as well as from other contaminants.

Purified BMP-6 bovine cartilage/bone protein
of the present invention are produced by culturing
25 a host cell transformed with a DNA sequence
comprising nucleotide #361 to nucleotide #666 as
set forth in Table II or substantially homologous
sequences and recovering from the culture medium a
protein comprising amino acid #121 to amino acid
30 #222 as set forth in Table II or a substantially
homologous sequence. In another embodiment the
bovine protein is produced by culturing a host cell
transformed with a sequence comprising nucleotide
#289 to #666 of Table II and recovering and
35 purifying a protein comprising amino acid #97 to

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amino acid #222. The purified BMP-6 bovine proteins are substantially free from other proteinaceous materials with which they are co-produced, as well as from other contaminants.

5 Purified human BMP-7 proteins may be produced by culturing a host cell transformed with the DNA sequence of Table V. The expressed proteins are isolated and purified from the culture medium. Purified human BMP-7 proteins are expected to be
10 characterized by an amino acid sequence comprising amino acid #300-#431 as shown in Table V. These purified BMP-7 human cartilage/bone proteins of the present invention are therefore produced by culturing a host cell transformed with a DNA
15 sequence comprising nucleotide #97 to nucleotide #1389 as shown in Table V or substantially homologous sequences operatively linked to a heterologous regulatory control sequence and recovering, isolating and purifying from the
20 culture medium a protein comprising the amino acid sequence as shown in Table V from amino acid #300 to amino acid #431 or a substantially homologous sequence.

Further emodiments may utilize the DNA
25 sequence comprising the nucleotides encoding amino acids #300 - #431. Purified BMP-7 proteins may be produced by culturing a host cell transformed with a DNA comprising the DNA sequence as shown in Table V from nucleotide #994 - #1389 or substantially
30 homologous sequences operatively linked to a heterologous regualtory control sequence and recovering, and purifying from the culture medium a protein comprising the amino acid sequence as shown in Table V from amino acid #300 to amino acid #431
35 or a substantially homologous sequence. The

purified human BMP-7 proteins are substantially free from other proteinaceous materials from which they are co-produced, as well as from other contaminants.

5 BMP-5, BMP-6 and BMP-7 proteins may be further characterized by the ability to demonstrate cartilage and/or bone formation activity. This activity may be demonstrated, for example, in the
10 rat bone formation assay as described in Example III. It is further contemplated that these proteins demonstrate activity in the assay at a concentration of 10 μ g - 500 lg/gram of bone formed. The proteins may be further characterized by the ability of 1 μ g to score at least +2 in this
15 assay using either the original or modified scoring method described further herein below.

BMP-5, BMP-6 and BMP-7 proteins may be further characterized by an apparent molecular weight of 28,000-30,000 daltons as determined by sodium
20 dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). Under reducing conditions in SDS-PAGE the protein electrophoresis with a molecular weight of approximately 14,000-20,000 daltons.

The proteins provided herein also include
25 factors encoded by the sequences similar to those of Tables I - V but into which modifications are naturally provided (e.g. allelic variations in the nucleotide sequence which may result in amino acid changes in the polypeptide) or deliberately
30 engineered. Similarly, synthetic polypeptides which wholly or partially duplicate continuous sequences of the amino acid residues of Tables I-V are encompassed by the invention. These sequences, by virtue of sharing primary, secondary,
35 or tertiary structural and conformational

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characteristics with other cartilage/bone proteins of the invention may possess bone and/or cartilage growth factor biological properties in common therewith. Thus, they may be employed as
5 biologically active substitutes for naturally-occurring proteins in therapeutic processes.

Other specific mutations of the sequences of the proteins of the invention described herein involve modifications of a glycosylation site.
10 These modification may involve O-linked or N-linked glycosylation sites. For instance, the absence of glycosylation or only partial glycosylation results from amino acid substitution or deletion at the asparagine-linked glycosylation recognition sites
15 present in the sequences of the proteins of the invention, as shown in Table I - V. The asparagine-linked glycosylation recognition sites comprise tripeptide sequences which are specifically recognized by appropriate cellular
20 glycosylation enzymes. These tripeptide sequences are either asparagine-X-threonine or asparagine-X-serine, where X is usually any amino acid. A variety of amino acid substitutions or deletions at one or both of the first or third amino acid
25 positions of a glycosylation recognition site (and/or amino acid deletion at the second position) results in non-glycosylation at the modified tripeptide sequence. Expression of such altered nucleotide sequences produces variants which are
30 not glycosylated at that site.

The present invention also encompasses the novel DNA sequences, free of association with DNA sequences encoding other proteinaceous materials, and coding on expression for the proteins of the
35 invention. These DNA sequences include those

depicted in Tables I - V in a 5' to 3' direction. Further included are those sequences which hybridize under stringent hybridization conditions [see, T. Maniatis et al, Molecular Cloning (A Laboratory Manual), Cold Spring Harbor Laboratory (1982), pages 387 to 389] to the DNA sequence of Tables I - V and demonstrate cartilage and/or bone formation activity in the rat bone formation assay. An example of one such stringent hybridization condition is hybridization at [6- 4 x SSC at 65°C, followed by a washing in 0.1 x SCC at 65°C for an hour. Alternatively, an exemplary stringent hybridization condition is in 50% formamide, 4 x SCC at 42°C.

Similarly, DNA sequences which encode proteins similar to the protein encoded by the sequences of Tables I - V, but which differ in codon sequence due to the degeneracies of the genetic code or allelic variations (naturally-occurring base changes in the species population which may or may not result in an amino acid change) also encode the proteins of the invention described herein. Variations in the DNA sequences of Tables I - V which are caused by point mutations or by induced modifications (including insertion, deletion, and substitution) to enhance the activity, half-life or production of the polypeptides encoded thereby are also encompassed in the invention.

In a further aspect, the invention provides a method for obtaining related human proteins or other mammalian BMP-5, BMP-6 and BMP-7 proteins. One method for obtaining such proteins entails, for instance, utilizing the human BMP-5, BMP-6 and BMP-7 coding sequence disclosed herein to probe a human genomic library using standard techniques for

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the human gene or fragments thereof. Sequences thus identified may also be used as probes to identify a human cell line or tissue which synthesizes the analogous cartilage/bone protein.

5 A cDNA library is synthesized and screened with probes derived from the human or bovine coding sequences. The human sequence thus identified is transformed into a host cell, the host cell is cultured and the protein recovered, isolated and

10 purified from the culture medium. The purified protein is predicted to exhibit cartilage and/or bone formation activity in the rat bone formation assay of Example III.

Another aspect of the present invention

15 provides a novel method for producing the BMP-5, BMP-6 and BMP-7 proteins of the invention. The method of the present invention involves culturing a suitable cell or cell line, which has been transformed with a DNA sequence as described above

20 coding for expression of a protein of the invention, under the control of known regulatory sequences. Regulatory sequences include promoter fragments, terminator fragments and other suitable sequences which direct the expression of the

25 protein in an appropriate host cell. Methods for culturing suitable cell lines are within the skill of the art. The transformed cells are cultured and the BMP proteins expressed thereby are recovered, isolated and purified from the culture medium

30 using purification techniques known to those skilled in the art. The purified BMP proteins are substantially free from other proteinaceous materials with which they are co-produced, as well as other contaminants. Purified BMP proteins of

35 the invention are substantially free from

materials with which the proteins of the invention exist in nature.

Suitable cells or cell lines may be mammalian cells, such as Chinese hamster ovary cells (CHO).
5 The selection of suitable mammalian host cells and methods for transformation, culture, amplification, screening and product production and purification are known in the art. See, e.g., Gething and Sambrook, Nature, 293:620-625 (1981), or
10 alternatively, Kaufman et al, Mol. Cell. Biol., 5(7):1750-1759 (1985) or Howley et al, U.S. Patent 4,419,446. Other suitable mammalian cell lines include but are not limited to the monkey COS-1 cell line and the CV-1 cell line.

15 Bacterial cells may also be suitable hosts. For example, the various strains of E. coli (e.g., HB101, MC1061) are well-known as host cells in the field of biotechnology. Various strains of B. subtilis, Pseudomonas, other bacilli and the
20 like may also be employed in this method.

Many strains of yeast cells known to those skilled in the art may also be available as host cells for expression of the polypeptides of the present invention. Additionally, where desired,
25 insect cells may be utilized as host cells in the method of the present invention. See, e.g. Miller et al, Genetic Engineering, 8:277-298 (Plenum Press 1986) and references cited therein.

Another aspect of the present invention
30 provides vectors for use in the method of expression of the proteins of the invention. The vectors contain the novel DNA sequences which code for the BMP-5, BMP-6 and BMP-7 proteins of the invention. Additionally, the vectors also contain
35 appropriate expression control sequences permitting

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expression of the protein sequences. Alternatively, vectors incorporating truncated or modified sequences as described above are also embodiments of the present invention and useful in the production of the proteins of the invention. The vectors may be employed in the method of transforming cell lines and contain selected regulatory sequences in operative association with the DNA coding sequences of the invention which are capable of directing the replication and expression thereof in selected host cells. Useful regulatory sequences for such vectors are known to those skilled in the art and may be selected depending upon the selected host cells. Such selection is routine and does not form part of the present invention. Host cells transformed with such vectors and progeny thereof for use in producing BMP-5, BMP-6 and BMP-7 proteins are also provided by the invention.

One skilled in the art can construct mammalian expression vectors by employing the DNA sequences of the invention and known vectors, such as pCD [Okayama et al., Mol. Cell Biol., 2:161-170 (1982)] and pJL3, pJL4 [Gough et al., EMBO J., 4:645-653 (1985)]. Similarly, one skilled in the art could manipulate the sequences of the invention by eliminating or replacing the mammalian regulatory sequences flanking the coding sequence with bacterial sequences to create bacterial vectors for intracellular or extracellular expression by bacterial cells. For example, the coding sequences could be further manipulated (e.g. ligated to other known linkers or modified by deleting non-coding sequences therefrom or altering nucleotides therein by other known

techniques). The modified coding sequence could then be inserted into a known bacterial vector using procedures such as described in T. Taniguchi et al., Proc. Natl Acad. Sci. USA, 77:5230-5233 (1980). This exemplary bacterial vector could then be transformed into bacterial host cells and a protein of the invention expressed thereby. For a strategy for producing extracellular expression of a cartilage and/or bone protein of the invention in bacterial cells., see, e.g. European patent application EPA 177,343.

Similar manipulations can be performed for the construction of an insect vector [See, e.g. procedures described in published European patent application 155,476] for expression in insect cells. A yeast vector could also be constructed employing yeast regulatory sequences for intracellular or extracellular expression of the factors of the present invention by yeast cells. [See, e.g., procedures described in published PCT application WO86/00639 and European patent application EPA 123,289].

A method for producing high levels of a protein of the invention from mammalian cells involves the construction of cells containing multiple copies of the heterologous gene encoding proteins of the invention. The heterologous gene may be linked to an amplifiable marker, e.g. the dihydrofolate reductase (DHFR) gene for which cells containing increased gene copies can be selected for propagation in increasing concentrations of methotrexate (MTX) according to the procedures of Kaufman and Sharp, J. Mol. Biol., 159:601-629 (1982). This approach can be employed with a number of different cell types.

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For instance, a plasmid containing a DNA sequence for a protein of the invention in operative association with other plasmid sequences enabling expression thereof and the DHFR expression plasmid pAdA26SV(A)3 [Kaufman and Sharp, Mol. Cell. Biol., 2:1304 (1982)] may be co-introduced into DHFR-deficient CHO cells, DUKX-BII, by calcium phosphate coprecipitation and transfection, electroporation or protoplast fusion.

DHFR expressing transformants are selected for growth in alpha media with dialyzed fetal calf serum, and subsequently selected for amplification by growth in increasing concentrations of MTX (sequential steps in 0.02, 0.2, 1.0 and 5uM MTX) as described in Kaufman et al., Mol Cell Biol., 5:1750 (1983). Protein expression should increase with increasing levels of MTX resistance.

Transformants are cloned, and the proteins of the invention are recovered, isolated, and purified from the culture medium. Characterization of expressed proteins may be carried out using standard techniques. For instance, characterization may include pulse labeling with [³⁵S] methionine or cysteine, or polyacrylamide gel electrophoresis. Biologically active protein expression is monitored by the Rosen-modified Sampath - Reddi rat bone formation assay described above in Example III. Similar procedures can be followed to produce other related proteins.

A protein of the present invention, which induces cartilage and/or bone formation in circumstances where bone and/or cartilage is not normally formed, has application in the healing of bone fractures and cartilage defects in humans and other animals. A preparation employing a protein

of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery. A protein of the invention may be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A variety of osteogenic, cartilage-inducing and bone inducing factors have been described. See, e.g. European Patent Applications 148,155 and 169,016 for discussions thereof.

The proteins of the invention may also be used in wound healing and related tissue repair. The types of wounds include, but are not limited to burns, incisions and ulcers. See, e.g. PCT Publication WO84/01106 for discussion of wound healing and related tissue repair.

A further aspect of the invention includes therapeutic methods and composition for repairing fractures and other conditions related to bone and/or cartilage defects or periodontal diseases. In addition, the invention comprises therapeutic methods and compositions for wound healing and tissue repair. Such compositions comprise a therapeutically effective amount of at least one of the BMP proteins BMP-5, BMP-6 and BMP-7 of the invention in admixture with a pharmaceutically acceptable vehicle, carrier or

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matrix.

It is expected that the proteins of the invention may act in concert with or perhaps synergistically with one another or with other
5 related proteins and growth factors. Therapeutic methods and compositions of the invention therefore comprise one or more of the proteins of the present invention. Further therapeutic methods and compositions of the invention therefore
10 comprise a therapeutic amount of at least one protein of the invention with a therapeutic amount of at least one of the other "BMP" proteins BMP-1, BMP-2, BMP-3 and BMP-4 disclosed in co-owned Published International Applications WO88/00205 and
15 WO89/10409 as mentioned above. Such methods and compositions of the invention may comprise proteins of the invention or portions thereof in combination with the above-mentioned "BMP" proteins or portions thereof.

20 Such combination may comprise individual separate molecules of the proteins or heteromolecules such as heterodimers formed by portions of the respective proteins. For example, a method and composition of the invention may
25 comprise a BMP protein of the present invention or a portion thereof linked with a portion of another "BMP" protein to form a heteromolecule.

Further therapeutic methods and compositions of the invention comprise the proteins of the
30 invention or portions thereof in combination with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF),
35 fibroblast growth factor (FGF), platelet derived

growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), K-fibroblast growth factor (KFGF), parathyroid hormone (PTH), leukemia inhibitory factor (LIF/HILDA, DIA) and insulin-like growth factor (IGF-I and IGF-II). Portions of these agents may also be used in compositions of the invention.

The preparation and formulation of such physiologically acceptable protein compositions, having due regard to pH, isotonicity, stability and the like, is within the skill of the art. The therapeutic compositions are also presently valuable for veterinary applications due to the apparent lack of species specificity in cartilage and bone growth factor proteins. Domestic animals and thoroughbred horses in addition to humans are desired patients for such treatment with the proteins of the present invention.

The therapeutic method includes administering the composition topically, systemically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of cartilage and/or bone or tissue damage. Topical administration may be suitable for wound healing and tissue repair.

Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the BMP proteins of the invention to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. The matrix may provide

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slow release of the BMP proteins or other factors comprising the composition. Such matrices may be formed of materials presently in use for other implanted medical applications.

- 5 The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions of the invention will define the
- 10 appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid and polyanhydrides. Other potential
- 15 materials are biodegradable and biologically well defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential
- 20 matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as
- 25 polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.
- 30 The dosage regimen will be determined by the attending physician considering various factors which modify the action of the proteins of the invention. Factors which may modify the action of the proteins of the invention include the amount of
- 35 bone weight desired to be formed, the site of bone

damage, the condition of the damaged bone, the size of a wound, type of damaged tissue, the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors.

5 The dosage may vary with the type of matrix used in the reconstitution and the type or types of bone and/or cartilage proteins present in the composition. The addition of other known growth factors, such as EGF, PDGF, TGF- α , TGF- β , and IGF-I
10 and IGF-II to the final composition, may also effect the dosage.

Progress can be monitored by periodic assessment of cartilage and/or bone growth and/or repair. The progress can be monitored, for
15 example, using x-rays, histomorphometric determinations and tetracycline labeling.

The following examples illustrate practice of the present invention in recovering and characterizing bovine cartilage and/or bone
20 proteins of the invention and employing these proteins to recover the corresponding human protein or proteins and in expressing the proteins via recombinant techniques.

EXAMPLE I

25 Isolation of Bovine Cartilage/Bone Inductive Protein

Ground bovine bone powder (20-120 mesh, Helitrex) is prepared according to the procedures of M. R. Urist et al., Proc. Natl Acad. Sci USA,
30 70:3511 (1973) with elimination of some extraction steps as identified below. Ten kgs of the ground powder is demineralized in successive changes of 0.6N

HCl at 4°C over a 48 hour period with vigorous

680 → 2201

stirring. The resulting suspension is extracted for 16 hours at 4°C with 50 liters of 2M CaCl_2 and 10mM ethylenediamine-tetraacetic acid [EDTA], and followed by extraction for 4 hours in 50 liters of 0.5M EDTA. The residue is washed three times with distilled water before its resuspension in 20 liters of 4M guanidine hydrochloride [GuCl], 20mM Tris (pH 7.4), 1mM N-ethylmaleimide, 1mM iodoacetamide, 1mM phenylmethylsulfonyl fluorine as described in Clin. Orthop. Rel. Res., 171: 213 (1982). After 16 to 20 hours the supernatant is removed and replaced with another 10 liters of GuCl buffer. The residue is extracted for another 24 hours.

The crude GuCl extracts are combined, concentrated approximately 20 times on a Pellicon apparatus with a 10,000 molecular weight cut-off membrane, and then dialyzed in 50mM Tris, 0.1M NaCl, 6M urea (pH 7.2), the starting buffer for the first column. After extensive dialysis the protein is loaded on a 4 liter DEAE cellulose column and the unbound fractions are collected.

The unbound fractions are concentrated and dialyzed against 50mM NaAc, 50mM NaCl (pH 4.6) in 6M urea. The unbound fractions are applied to a carboxymethyl cellulose column. Protein not bound to the column is removed by extensive washing with starting buffer, and the material containing protein having bone and/or cartilage formation activity as measured by the Rosen-modified Sampath-Reddi assay (described in Example III below) desorbed from the column by 50mM NaAc, 0.25mM NaCl, 6M urea (pH 4.6). The protein from this step elution is concentrated 20- to 40- fold, then diluted 5 times with 80mM KPO_4 , 6M urea (pH 6.0).

The pH of the solution is adjusted to 6.0 with 500mM K_2HPO_4 . The sample is applied to an hydroxylapatite column (LKB) equilibrated in 80mM KPO_4 , 6M urea (pH6.0) and all unbound protein is removed by washing the column with the same buffer. Protein having bone and/or cartilage formation activity is eluted with 100mM KPO_4 (pH7.4) and 6M urea.

The protein is concentrated approximately 10 times, and solid NaCl added to a final concentration of 0.15M. This material is applied to a heparin - Sepharose column equilibrated in 50mM KPO_4 , 150mM NaCl, 6M urea (pH7.4). After extensive washing of the column with starting buffer, a protein with bone and/or cartilage inductive activity is eluted by 50mM KPO_4 , 700mM NaCl, 6M urea (pH7.4). This fraction is concentrated to a minimum volume, and 0.4ml aliquots are applied to Superose 6 and Superose 12 columns connected in series, equilibrated with 4M GuCl, 20mM Tris (pH7.2) and the columns developed at a flow rate of 0.25ml/min. The protein demonstrating bone and/or cartilage inductive activity corresponds to an approximate 30,000 dalton protein.

The above fractions from the superose columns are pooled, dialyzed against 50mM NaAc, 6M urea (pH4.6), and applied to a Pharmacia MonoS HR column. The column is developed with a gradient to 1.0M NaCl, 50mM NaAc, 6M urea (pH4.6). Active bone and/or cartilage formation fractions are pooled. The material is applied to a 0.46 x 25cm Vydac C4 column in 0.1% TFA and the column developed with a gradient to 90% acetonitrile, 0.1% TFA (31.5% acetonitrile, 0.1% TFA to 49.5% acetonitrile, 0.1% TFA in 60 minutes at 1ml per minute). Active

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material is eluted at approximately 40-44% acetonitrile. Fractions were assayed for cartilage and/or bone formation activity. The active material is further fractionated on a MonoQ column. The protein is dialyzed against 6M urea, 25mM diethanolamine, pH 8.6 and then applied to a 0.5 by 5 cm MonoQ column (Pharmacia) which is developed with a gradient of 6M urea, 25mM diethanolamine, pH 8.6 and 0.5 M NaCl, 6M urea, 25mM diethanolamine, pH 8.6. Fractions are brought to pH 3.0 with 10% trifluoroacetic acid (TFA). Aliquots of the appropriate fractions are iodinated by one of the following methods: P. J. McConahey et al, Int. Arch. Allergy, 29:185-189 (1966); A. E. Bolton et al, Biochem J., 133:529 (1973); and D. F. Bowen-Pope, J. Biol. Chem., 237:5161 (1982). The iodinated proteins present in these fractions are analyzed by SDS gel electrophoresis.

EXAMPLE II

20 Characterization of Bovine Cartilage/Bone Inductive Factor

A. Molecular Weight

Approximately 5 μ g protein from Example I in 6M urea, 25mM diethanolamine, pH 8.6, approximately 0.3 M NaCl is made 0.1% with respect to SDS and dialyzed against 50 mM tris/HCl 0.1% SDS pH 7.5 for 16 hrs. The dialyzed material is then electrophoretically concentrated against a dialysis membrane [Hunkapillar et al Meth. Enzymol. 91: 227-236 (1983)] with a small amount of I 125 labelled counterpart. This material (volume approximately 100 μ l) is loaded onto a 12% polyacrylamide gel and subjected to SDS-PAGE [Laemmli, U.K. Nature, 227:680-685 (1970)] without

reducing the sample with dithiothreitol. The molecular weight is determined relative to prestained molecular weight standards (Bethesda Research Labs). Following autoradiography of the unfixed gel the approximate 28,000-30,000 dalton band is excised and the protein electrophoretically eluted from the gel (Hunkapillar et al supra). Based on similar purified bone fractions as described in the co-pending "BMP" applications described above wherein bone and/or cartilage activity is found in the 28,000-30,000 region, it is inferred that this band comprises bone and/or cartilage inductive fractions.

B. Subunit Characterization

The subunit composition of the isolated bovine bone protein is also determined. The eluted protein described above is fully reduced and alkylated in 2% SDS using iodoacetate and standard procedures and reconcentrated by electrophoretic packing. The fully reduced and alkylated sample is then further submitted to SDS-PAGE on a 12% gel and the resulting approximate 14,000-20,000 dalton region having a doublet appearance located by autoradiography of the unfixed gel. A faint band remains at the 28,000-30,000 region. Thus the 28,000-30,000 dalton protein yields a broad region of 14,000-20,000 which may otherwise also be interpreted and described as comprising two broad bands of approximately 14,000-16,000 and 16,000-20,000 daltons.

EXAMPLE III

Rosen Modified Sampath-Reddi Assay

A modified version of the rat bone

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formation assay described in Sampath and Reddi, Proc. Natl. Acad. Sci. U.S.A., 80:6591-6595 (1983) is used to evaluate bone and/or cartilage activity of the proteins of the invention. This modified assay is herein called the Rosen-modified Sampath-Reddi assay. The ethanol precipitation step of the Sampath-Reddi procedure is replaced by dialyzing (if the composition is a solution) or diafiltering (if the composition is a suspension) the fraction to be assayed against water. The solution or suspension is then redissolved in 0.1 % TFA, and the resulting solution added to 20mg of rat matrix. A mock rat matrix sample not treated with the protein serves as a control. This material is frozen and lyophilized and the resulting powder enclosed in #5 gelatin capsules. The capsules are implanted subcutaneously in the abdominal thoracic area of 21 - 49 day old male Long Evans rats. The implants are removed after 7 - 14 days. Half of each implant is used for alkaline phosphatase analysis [See, A. H. Reddi et al., Proc. Natl Acad Sci., 69:1601 (1972)].

The other half of each implant is fixed and processed for histological analysis. Glycolmethacrylate sections (1 μ m) are stained with Von Kossa and acid fuschin or toluidine blue to score the amount of induced bone and cartilage formation present in each implant. The terms +1 through +5 represent the area of each histological section of an implant occupied by new bone and/or cartilage cells and newly formed bone and matrix. Two scoring methods are herein described. In the first scoring method a score of +5 indicates that greater than 50% of the implant is new bone and/or cartilage produced as a direct result of protein in

the implant. A score of +4, +3, +2 and +1 would indicate that greater than 40%, 30%, 20% and 10% respectively of the implant contains new cartilage and/or bone. The second scoring method (which hereinafter may be referred to as the modified scoring method) is as follows: three non-adjacent sections are evaluated from each implant and averaged. "+/-" indicates tentative identification of cartilage or bone; "+1" indicates >10% of each section being new cartilage or bone; "+2", >25%; "+3", >50%; "+4", >75%; "+5", >80%. The scores of the individual implants are tabulated to indicate assay variability.

It is contemplated that the dose response nature of the cartilage and/or bone inductive protein containing samples of the matrix samples will demonstrate that the amount of bone and/or cartilage formed increases with the amount of cartilage/bone inductive protein in the sample. It is contemplated that the control samples will not result in any bone and/or cartilage formation.

As with other cartilage and/or bone inductive proteins such as the above-mentioned "BMP" proteins, the bone and/or cartilage formed is expected to be physically confined to the space occupied by the matrix. Samples are also analyzed by SDS gel electrophoresis and isoelectric focusing followed by autoradiography. The activity is correlated with the protein bands and pI. To estimate the purity of the protein in a particular fraction an extinction coefficient of 1 OD/mg-cm is used as an estimate for protein and the protein is run on SDS-PAGE followed by silver staining or radioiodination and autoradiography.

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EXAMPLE IV

A. Bovine Protein Composition

The gel slice of the approximate 14,000-20,000 dalton region described in Example IIB is fixed with methanol-acetic acid-water using standard procedures, briefly rinsed with water, then neutralized with 0.1M ammonium bicarbonate. Following dicing the gel slice with a razor blade, the protein is digested from the gel matrix by adding 0.2 μ g of TPCCK-treated trypsin (Worthington) and incubating the gel for 16 hr. at 37 degrees centigrade. The resultant digest is then subjected to RPHPLC using a C4 Vydac RPHPLC column and 0.1% TFA-water 0.1% TFA water-acetonitrile gradient. The resultant peptide peaks were monitored by UV absorbance at 214 and 280 nm and subjected to direct amino terminal amino acid sequence analysis using an Applied Biosystems gas phase sequenator (Model 470A). One tryptic fragment is isolated by standard procedures having the following amino acid sequence as represented by the amino acid standard three-letter symbols and where "Xaa" indicates an unknown amino acid the amino acid in parentheses indicates uncertainty in the sequence:

Xaa-His-Glu-Leu-Tyr-Val-Ser-Phe-(Ser)

The following four oligonucleotide probes are designed on the basis of the amino acid sequence of the above-identified tryptic fragment and synthesized on an automated DNA synthesizer.

PROBE #1: GTRCTYGANATRCANTC

PROBE #2: GTRCTYGANATRCANAG

PROBE #3: GTRCTYAAAYATRCANTC

PROBE #4: GTRCTYAAAYATRCANAG

5 The standard nucleotide symbols in the above identified probes are as follows: A,adenosine; C,cytosine; G,guanine; T,thymine; N, adenosine or cytosine or guanine or thymine; R,adenosine or guanine; and Y,cytosine or thymine.

10 Each of the probes consists of pools of oligonucleotides. Because the genetic code is degenerate (more than one codon can code for the same amino acid), a mixture of oligonucleotides is synthesized that contains all possible nucleotide sequences encoding the amino acid sequence of the tryptic. These probes are radioactively labeled and employed to screen a bovine cDNA library as described below.

B. Bovine BMP-5

20 Poly(A) containing RNA is isolated by oligo(dT) cellulose chromatography from total RNA isolated from fetal bovine bone cells by the method of Gehron-Robey et al in Current Advances in Skeletogenesis, Elsevier Science Publishers (1985). The total RNA was obtained from Dr. Marion Young, National Institute of Dental Research, National Institutes of Health. A cDNA library is made in lambda gt10 (Toole et al supra) and plated on 50 plates at 8000 recombinants per plate. These recombinants (400,000) are screened on duplicate nitrocellulose filters with a combination of Probes 25 1, 2, 3, and 4 using the Tetramethylammonium chloride (TMAC) hybridization procedure [see Wozney et al Science, 242: 1528-1534 (1988)]. Twenty-

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eight positives are obtained and are replated for secondaries. Duplicate nitrocellulose replicas again are made. One set of filters are screened with Probes #1 and #2; the other with Probes #3 and #4. Six positives are obtained on the former, 21 positives with the latter. One of the six, called HEL5, is plaque purified, a phage plate stock made, and bacteriophage DNA isolated. This DNA is digested with EcoRI and subcloned into M13 and pSP65 (Promega Biotec, Madison, Wisconsin) [Melton, et al. Nucl. Acids Res. 12: 7035-7056 (1984)]. The DNA sequence and derived amino acid sequence of this fragment is shown in Table I.

DNA sequence analysis of this fragment in M13 indicates that it encodes the desired tryptic peptide sequence set forth above, and this derived amino acid sequence is preceded by a basic residue (Lys) as predicted by the specificity of trypsin. The underlined portion of the sequence in Table I from amino acid #42 to #48 corresponds to the tryptic fragment identified above from which the oligonucleotide probes are designed. The derived amino acid sequence Ser-Gly-Ser-His-Gln-Asp-Ser-Ser-Arg as set forth in Table I from amino acid #15 to #23 is noted to be similar to a tryptic fragment sequence Ser-Thr-Pro-Ala-Gln-Asp-Val-Ser-Arg found in the 28,000 - 30,000 dalton purified bone preparation as described in the "BMP" Publications WO88/00205 and WO89/10409 mentioned above. This fragment set forth in Table I is a portion of the DNA sequence which encodes a bovine BMP-5 protein. The DNA sequence shown in Table I indicates an open reading frame from the 5' end of the clone of 420 base pairs, encoding a partial peptide of 140 amino acid residues (the first 7 nucleotides are of the

TABLE I

1	TCTAGAGGTGAGAGCAGCCAACAAGAGAAAAAATCAAACCGCAATAAATCCGGCTCTCAT LeuGluValArgAlaAlaAsnLysArgLysAsnGlnAsnArgAsnLys <u>SerGlySerHis</u> (1) (15)	61
62	CAGGACTCCTCTAGAATGTCCAGTGTGGAGATTATAACACCAGTGAACAAAAACAAGCC <u>GlnAspSerSerArg</u> MetSerSerValGlyAspTyrAsnThrSerGluGlnLysGlnAla (23)	12
122	TGTA AAAAGCATGAACTCTATGTGAGTTTCCGGGATCTGGGATGGCAGGACTGGATTATA CysLysLys <u>HisGluLeuTyrValSerPhe</u> ArgAspLeuGlyTrpGlnAspTrpIleIle (42) (48)	18
182	GCACCAGAAGGATATGCTGCATTTTATTGTGATGGAGAATGTTCTTTTCCACTCAATGCC AlaProGluGlyTyrAlaAlaPheTyrCysAspGlyGluCysSerPheProLeuAsnAla	24
242	CATATGAATGCCACCAATCATGCCATAGTTCAGACTCTGGTTCACCTGATGTTTCCTGAC HisMetAsnAlaThrAsnHisAlaIleValGlnThrLeuValHisLeuMetPheProAsp	30
302	CACGTACCAAAGCCTTGCTGCGCGACAAACAACTAAATGCCATCTCTGTGTTGTACTTT HisValProLysProCysCysAlaThrAsnLysLeuAsnAlaIleSerValLeuTyrPhe	36
362	GATGACAGCTCCAATGTCATTTTGAAAAAGTACAGAAATATGGTCGTGCGTTTCGTGTGGT AspAspSerSerAsnValIleLeuLysLysTyrArgAsnMetValValArgSerCysGly	42
422	TGCCACTAATAGTGCATAATAATGGTAATAAGAAAAAAGATCTGTATGGAGGTTTATGA CysHisEnd (140)	48
481	CTACAATAAAAAATATCTTTTCGGATAAAAGGGGAATTTAATAAAATTAGTCTGGCTCATT	54
541	TCATCTCTGTAACCTATGTACAAGAGCATGTATATAGT	578

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adaptors used in the cloning procedure). An in-frame stop codon (TAA) indicates that this clone encodes the carboxy-terminal part of bovine BMP-5.

C. Bovine BMP-6

The remaining positive clones (the second set containing 21 positives) isolated with Probes #1, #2, #3, and #4 described above are screened with HEL5 and a further clone is identified that hybridizes under reduced hybridization conditions [5x SSC, 0.1% SDS, 5X Denhardt's, 100 µg/ml salmon sperm DNA standard hybridization buffer (SHB) at 65°C, wash in 2XSSC 0.1% SDS at 65°C]. This clone is plaque purified, a phage plate stock made and bacteriophage DNA isolated. The DNA sequence and derived amino acid sequence of a portion of this clone is shown in Table II. This sequence represents a portion of the DNA sequence encoding a bovine BMP-6 cartilage/bone protein of the invention.

The first underlined portion of the sequence in Table II from amino acid #97 - amino acid #105 corresponds to the tryptic fragment found in the 28,000-30,000 dalton purified bovine bone preparation (and its reduced form at approximately 18,000-20,000 dalton reduced form) as described in the "BMP" Publications WO88/00205 and WO89/10409 mentioned above. The second underlined sequence in Table II from amino acid #124 - amino acid #130 corresponds to the tryptic fragment identified above from which the oligonucleotide probes are designed.

The DNA sequence of Table II indicates an open reading frame of 666 base pairs starting from the 5' end of the sequence of Table II, encoding a partial peptide of 222 amino acid residues. An in-frame stop codon (TGA) indicates that this clone encodes the carboxy-terminal part of a bovine BMP-6

606-70 ✓

protein. Based on knowledge of other BMP proteins and other proteins in the TGF- β family, it is predicted that the precursor polypeptide would be cleaved at the three basic residues (ArgArgArg) to yield a mature peptide beginning with residue 90 or 91 of the sequence of Table II.

5

TABLE II

9			18			27			36			45			54					
CTG	CTG	GGC	ACG	CGT	GCT	GTG	TGG	GCC	TCA	GAG	GCG	GGC	TGG	CTG	GAG	TTT	GAC			
Leu	Leu	Gly	Thr	Arg	Ala	Val	Trp	Ala	Ser	Glu	Ala	Gly	Trp	Leu	Glu	Phe	Asp			
(1)			63			72			81			90			99			108		
ATC	ACG	GCC	ACC	AGC	AAC	CTG	TGG	GTC	CTG	ACT	CCG	CAG	CAC	AAC	ATG	GGG	CTG			
Ile	Thr	Ala	Thr	Ser	Asn	Leu	Trp	Val	Leu	Thr	Pro	Gln	His	Asn	MET	Gly	Leu			
117			126			135			144			153			162					
CAG	CTG	AGC	GTG	GTC	ACG	CGT	GAT	GGG	CTC	AGC	ATC	AGC	CCT	GGG	GCC	GCG	GGC			
Gln	Leu	Ser	Val	Val	Thr	Arg	Asp	Gly	Leu	Ser	Ile	Ser	Pro	Gly	Ala	Ala	Gly			
171			180			189			198			207			216					
CTG	GTG	GGC	AGG	GAC	GGC	CCC	TAC	GAC	AAG	CAG	CCC	TTC	ATG	GTG	GCC	TTC	TTC			
Leu	Val	Gly	Arg	Asp	Gly	Pro	Tyr	Asp	Lys	Gln	Pro	Phe	MET	Val	Ala	Phe	Phe			
225			234			243			252			261			270					
AAG	GCC	AGT	GAG	GTC	CAC	GTG	CGC	AGT	GCC	CGG	TGG	GCC	CCC	GGG	CGG	CGC	CGG			
Lys	Ala	Ser	Glu	Val	His	Val	Arg	Ser	Ala	Arg	Ser	Ala	Pro	Gly	Arg	Arg	Arg			
279			288			297			306			315			324					
CAG	CAG	GCC	CGG	AAC	CGC	TCC	ACC	CCG	GCC	CAG	GAC	GTG	TGG	CGG	GCC	TCC	AGC			
Gln	Gln	Ala	Arg	Asn	Arg	<u>Ser</u>	<u>Thr</u>	<u>Pro</u>	<u>Ala</u>	<u>Gln</u>	<u>Asp</u>	<u>Val</u>	<u>Ser</u>	<u>Arg</u>	<u>Ala</u>	<u>Ser</u>	<u>Ser</u>			
333			342			351			360			369			378					
						(97)									(105)					
GCC	TCA	GAC	TAC	AAC	AGC	AGC	GAG	CTG	AAG	ACG	GCC	TGC	CGG	AAG	CAT	GAG	CTC			
Ala	Ser	Asp	Tyr	Asn	Ser	Ser	Glu	Leu	Lys	Thr	Ala	Cys	Arg	Lys	<u>His</u>	<u>Glu</u>	<u>Leu</u>			
387			396			405			414			423			432					
									(121)			(124)								
TAC	GTG	AGC	TTC	CAG	GAC	CTG	GGG	TGG	CAG	GAC	TGG	ATC	ATT	GCC	CCC	AAG	GGC			
<u>Tyr</u>	<u>Val</u>	<u>Ser</u>	<u>Phe</u>	<u>Gln</u>	<u>Asp</u>	<u>Leu</u>	<u>Gly</u>	<u>Trp</u>	<u>Gln</u>	<u>Asp</u>	<u>Trp</u>	<u>Ile</u>	<u>Ile</u>	<u>Ala</u>	<u>Pro</u>	<u>Lys</u>	<u>Gly</u>			
441			450			459			468			477			486					
TAC	GCT	GCC	AAC	TAC	TGT	GAC	GGA	GAA	TGT	TGG	TTC	CCT	CTC	AAC	GCA	CAC	ATG			
Tyr	Ala	Ala	Asn	Tyr	Cys	Asp	Gly	Glu	Cys	Ser	Phe	Pro	Leu	Asn	Ala	His	MET			
495			504			513			522			531			540					
AAC	GCT	ACC	AAC	CAT	GCC	ATC	GTG	CAG	ACC	CTG	GTT	CAC	CTC	ATG	AAC	CCC	GAG			
Asn	Ala	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	His	Leu	MET	Asn	Pro	Glu			

607-70dc

TABLE II
(page 2 of 2)

549	558	567	576	585	594
TAC GTC CCC AAA CCG TGC TGC GCG CCC ACG AAA CTG AAC GGC ATC TCG GTG CTC					
Tyr Val Pro Lys Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu					
603	612	621	630	639	648
TAC TTC GAC GAC AAC TCC AAT GTC ATC CTG AAG AAG TAC CCG AAC ATG GTC GTA					
Tyr Phe Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn MET Val Val					
657	666	676	686	696	706
716					
CGA GCG TGT GGG TGC CAC TGA CTGGGGG TGAGTGGCTG GGGAGGCTGT GCACACACTG CCTGGACTCC					
Arg Ala Cys Gly Cys His					
(222)					
726	736	746	756	766	776
786					
TGGATCAAGT CCGCTTTAAG CCCACAGAGG CCCCCGGGAC ACAGGAGGAG ACCCCGAGGC CACCTTGGGC					
796	806	816	826	836	846
856					
TGGGGTTGGC CTTTCCGGCC AACGCAGAAC CGAAGGGAAC CTGTCCGGCC CTTGCTCACA CCGTGAGCGT					
866	876	886			
TGTGAGTAGC CATCGGGCTC TAGGAAGCAG CACTCGAG					

EXAMPLE V

A. Human Protein Composition

Human cell lines which synthesize BMP-5 and/or BMP-6 mRNAs are identified in the following manner. RNA is isolated from a variety of human cell lines, selected for poly(A)-containing RNA by chromatography on oligo(dT) cellulose, electrophoresed on a formaldehyde-agarose gel, and transferred to nitrocellulose. A nitrocellulose replica of the gel is hybridized to a single stranded M13 ³²P-labeled probe corresponding to the above mentioned BMP-5 EcoRI-BglII fragment containing nucleotides 1-465 of the sequence of Table I. A strongly hybridizing band is detected in the lane corresponding to the human osteosarcoma cell line U-2OS RNA. Another nitrocellulose replica is hybridized to a single stranded M13 ³²P-labeled probe containing the PstI-SmaI fragment of bovine BMP-6 (corresponding to nucleotides 106-261 of Table II). It is found that several RNA species in the lane corresponding to U-2OS RNA hybridize to this probe.

A cDNA Library is made in the vector lambda ZAP (Stratagene) from U-2OS poly(A)-containing RNA using established techniques (Toole et al.). 750,000 recombinants of this library are plated and duplicate nitrocellulose replicas made. The SmaI fragment of bovine BMP-6 corresponding to nucleotides 259-751 of Table II is labeled by nick-translation and hybridized to both sets of filters in SHB at 65°C. One set of filters is washed under stringent conditions (0.2X SSC, 0.1% SDS at 65°C), the other under reduced stringency conditions (1X SSC, 0.1% SDS at 65°C). Many

608-7000

duplicate hybridizing recombinants (approximately 162) are noted. 24 are picked and replated for secondaries. Three nitrocellulose replicas are made of each plate. One is hybridized to the BMP-6 SmaI probe, one to a nick-translated BMP-6 PstI-SacI fragment (nucleotides 106-378 of Table II), and the third to the nick-translated BMP-5 XbaI fragments (nucleotides 1-76 of Table I). Hybridization and washes are carried out under stringent conditions.

B. Human BMP-5 Proteins

17 clones that hybridize to the third probe more strongly than to the second probe are plaque purified. DNA sequence analysis of one of these, U2-16, indicates that it encodes human BMP-5. U2-16 was deposited with the American Type Culture Collection (ATCC), Rockville, Maryland on June 22, 1989 under accession number ATCC 68109. This deposit as well as the other deposits described herein are made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure and the Regulations thereunder (Budapest Treaty). U2-16 contains an insert of approximately 2.1 Kb. The DNA sequence and derived amino acid sequence of U2-16 is shown below in Table III. This clone is expected to contain all of the nucleotide sequence necessary to encode human BMP-5 proteins. The cDNA sequence of Table III contains an open reading frame of 1362 bp, encoding a protein of 454 amino acids, preceded by a 5' untranslated region of 700 bp with stop codons in all frames, and contains a 3' untranslated region of 90 bp following the in frame stop codon (TAA).

5 This protein of 454 amino acids has a
molecular weight of approximately 52,000 daltons as
predicted by its amino acid sequence, and is
contemplated to represent the primary translation
product. Based on knowledge of other BMP proteins
and other proteins within the TGF- β family, it is
predicted that the precursor polypeptide would be
cleaved at the tribasic peptide Lys Arg Lys
yielding a 132 amino acid mature peptide beginning
10 with amino acid #323 "Asn". The processing of BMP-
5 into the mature form is expected to involve
dimerization and removal of the N-terminal region
in a manner analogous to the processing of the
related protein TGF- β [L.E. Gentry, et al., Molec.
15 & Cell. Biol. 8:4162 (1988); R. Dernyck, et al.,
Nature 316:701 (1985)].

It is contemplated therefore that the mature
active species of BMP-5 comprises a homodimer of 2
polypeptide subunits each subunit comprising amino
20 acid #323 - #454 with a predicted molecular weight
of approximately 15,000 daltons. Further active
BMP-5 species are contemplated, for example,
proprotein dimers or proprotein subunits linked to
mature subunits. Additional active species may
25 comprise amino acid #329 - #454 such species
including homologous the tryptic sequences found in
the purified bovine material. Also contemplated
are BMP-5 proteins comprising amino acids #353-
#454 thereby including the first conserved
30 cysteine residue.

The underlined sequence of Table III from
amino acid #329 to #337 Ser-Ser-Ser-His-Gln-Asp-
Ser-Ser-Arg shares homology with the bovine
sequence of Table I from amino acid #15 to #23 as
35 discussed above in Example IV. Each of these

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sequences shares homology with a tryptic fragment
sequence Ser-Thr-Pro-Ala-Gln-Asp-Val-Ser-Arg found
in the 28,000 - 30,000 dalton purified bone
preparation (and its reduced form at approximately
5 18,000 - 20,000 daltons) as described in the "BMP"
published applications WO88/00205 and WO89/10409
mentioned above.

The underlined sequence of Table III from
amino acid #356 to #362 His-Glu-Leu-Tyr-Val-Ser-Phe
10 corresponds to the tryptic fragment identified in
the bovine bone preparation described above from
which the oligonucleotide probes are designed.

TABLE III

10	20	30	40	50
CTGGTATATT	TGTGCCTGCT	GGAGGTGGAA	TTAACAGTAA	GAAGGAGAAA
60	70	80	90	100
GGGATTGAAT	GGACTTACAG	GAAGGATTTC	AAGTAAATTC	AGGGAAACAC
110	120	130	140	150
ATTTACTTGA	ATAGTACAAC	CTAGAGTATT	ATTTTACACT	AAGACGACAC
160	170	180	190	200
AAAAGATGTT	AAAGTTATCA	CCAAGCTGCC	GGACAGATAT	ATATTCCAAC
210	220	230	240	250
ACCAAGGTGC	AGATCAGCAT	AGATCTGTGA	TTCAGAAATC	AGGATTTGTT
260	270	280	290	300
TTGGAAAGAG	CTCAAGGGTT	GAGAAGAACT	CAAAAGCAAG	TGAAGATTAC
310	320	330	340	350
TTTGGGAACT	ACAGTTTATC	AGAAGATCAA	CTTTTGCTAA	TTCAAATACC
360	370	380	390	400
AAAGGCCTGA	TTATCATAAA	TTCATATAGG	AATGCATAGG	TCATCTGATC
410	420	430	440	450
AAATAATATT	AGCCGTCTTC	TGCTACATCA	ATGCAGCAAA	AACTCTTAAC
460	470	480	490	500
AACTGTGGAT	AATTGGAAAT	CTGAGTTTCA	GCTTTCTTAG	AAATAACTAC
510	520	530	540	550
TCTTGACATA	TTCCAAAATA	TTTAAAATAG	GACAGGAAAA	TCGGTGAGGA
560	570	580	590	600
TGTTGTGCTC	AGAAATGTCA	CTGTCATGAA	AAATAGGTAA	ATTTGTTTTT
610	620	630	640	650
TCAGCTACTG	GGAAACTGTA	CCTCCTAGAA	CCTTAGGTTT	TTTTTTTTTT
660	670	680	690	700
AAGAGGACAA	GAAGGACTAA	AAATATCAAC	TTTTGCTTTT	GGACAAAA

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TABLE III
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701	710	719	728	737
ATG CAT CTG ACT GTA TTT TTA CTT AAG GGT ATT GTG GGT TTC CTC				
MET His Leu Thr Val Phe Leu Leu Lys Gly Ile Val Gly Phe Leu				
(1)				
746	755	764	773	782
TGG AGC TGC TGG GTT CTA GTG GGT TAT GCA AAA GGA GGT TTG GGA				
Trp Ser Cys Trp Val Leu Val Gly Tyr Ala Lys Gly Gly Leu Gly				
791	800	809	818	827
GAC AAT CAT GTT CAC TCC AGT TTT ATT TAT AGA AGA CTA CGG AAC				
Asp Asn His Val His Ser Ser Phe Ile Tyr Arg Arg Leu Arg Asn				
836	845	854	863	872
CAC GAA AGA CGG GAA ATA CAA AGG GAA ATT CTC TCT ATC TTG GGT				
His Glu Arg Arg Glu Ile Gln Arg Glu Ile Leu Ser Ile Leu Gly				
881	890	899	908	917
TTG CCT CAC AGA CCC AGA CCA TTT TCA CCT GGA AAA ATG ACC AAT				
Leu Pro His Arg Pro Arg Pro Phe Ser Pro Gly Lys Gln Ala Ser				
926	935	944	953	962
CAA GCG TCC TCT GCA CCT CTC TTT ATG CTG GAT CTC TAC AAT GCC				
Ser Ala Pro Leu Phe MET Leu Asp Leu Tyr Asn Ala MET Thr Asn				
971	980	989	998	1007
GAA GAA AAT CCT GAA GAG TCG GAG TAC TCA GTA AGG GCA TCC TTG				
Glu Glu Asn Pro Glu Glu Ser Glu Tyr Ser Val Arg Ala Ser Leu				
1016	1025	1034	1043	1052
GCA GAA GAG ACC AGA GGG GCA AGA AAG GGA TAC CCA GCC TCT CCC				
Ala Glu Glu Thr Arg Gly Ala Arg Lys Gly Tyr Pro Ala Ser Pro				
1061	1070	1079	1088	1097
AAT GGG TAT CCT CGT CGC ATA CAG TTA TCT CGG ACG ACT CCT CTG				
Asn Gly Tyr Pro Arg Arg Ile Gln Leu Ser Arg Thr Thr Pro Leu				
1106	1115	1124	1133	1142
ACC ACC CAG AGT CCT CCT CTA GCC AGC CTC CAT GAT ACC AAC TTT				
Thr Thr Gln Ser Pro Pro Leu Ala Ser Leu His Asp Thr Asn Phe				
1151	1160	1169	1178	1187
CTG AAT GAT GCT GAC ATG GTC ATG AGC TTT GTC AAC TTA GTT GAA				
Leu Asn Asp Ala Asp MET Val MET Ser Phe Val Asn Leu Val Glu				
1196	1205	1214	1223	1232
AGA GAC AAG GAT TTT TCT CAC CAG CGA AGG CAT TAC AAA GAA TTT				
Arg Asp Lys Asp Phe Ser His Gln Arg Arg His Tyr Lys Glu Phe				

TABLE III
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1241	1250	1259	1268	1277
CGA TTT GAT CTT ACC CAA ATT CCT CAT GGA GAG GCA GTG ACA GCA				
Arg Phe Asp Leu Thr Gln Ile Pro His Gly Glu Ala Val Thr Ala				
1286	1295	1304	1313	1322
GCT GAA TTC CGG ATA TAC AAG GAC CGG AGC AAC AAC CGA TTT GAA				
Ala Glu Phe Arg Ile Tyr Lys Asp Arg Ser Asn Asn Arg Phe Glu				
1331	1340	1349	1358	1367
AAT GAA ACA ATT AAG ATT AGC ATA TAT CAA ATC ATC AAG GAA TAC				
Asn Glu Thr Ile Lys Ile Ser Ile Tyr Gln Ile Ile Lys Glu Tyr				
1376	1385	1394	1403	1412
ACA AAT AGG GAT GCA GAT CTG TTC TTG TTA GAC ACA AGA AAG GCC				
Thr Asn Arg Asp Ala Asp Leu Phe Leu Leu Asp Thr Arg Lys Ala				
1421	1430	1439	1448	1457
CAA GCT TTA GAT GTG GGT TGG CTT GTC TTT GAT ATC ACT GTG ACC				
Gln Ala Leu Asp Val Gly Trp Leu Val Phe Asp Ile Thr Val Thr				
1466	1475	1484	1493	1502
AGC AAT CAT TGG GTG ATT AAT CCC CAG AAT AAT TTG GGC TTA CAG				
Ser Asn His Trp Val Ile Asn Pro Gln Asn Asn Leu Gly Leu Gln				
1511	1520	1529	1538	1547
CTC TGT GCA GAA ACA GGG GAT GGA CGC AGT ATC AAC GTA AAA TCT				
Leu Cys Ala Glu Thr Gly Asp Gly Arg Ser Ile Asn Val Lys Ser				
1556	1565	1574	1583	1592
GCT GGT CTT GTG GGA AGA CAG GGA CCT CAG TCA AAA CAA CCA TTC				
Ala Gly Leu Val Gly Arg Gln Gly Pro Gln Ser Lys Gln Pro Phe				
1601	1610	1619	1628	1637
ATG GTG GCC TTC TTC AAG GCG AGT GAG GTA CTT CTT CGA TCC GTG				
MET Val Ala Phe Phe Lys Ala Ser Glu Val Leu Leu Arg Ser Val				
1646	1655	1664	1673	1682
AGA GCA GCC AAC AAA CGA AAA AAT CAA AAC CGC AAT AAA TCC AGC				
Arg Ala Ala Asn Lys Arg Lys Asn Gln Asn Arg Asn Lys <u>Ser Ser</u>				
		(323)		(329)
1691	1700	1709	1718	1727
TCT CAT CAG GAC TCC TCC AGA ATG TCC AGT GTT GGA GAT TAT AAC				
<u>Ser His Gln Asp Ser Ser Arg</u> MET Ser Ser Val Gly Asp Tyr Asn				
		(337)		

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TABLE III
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1736	1745	1754	1763	1772	
ACA AGT GAG CAA AAA CAA GCC TGT AAG AAG CAC GAA CTC TAT GTG					
Thr Ser Glu Gln Lys Gln Ala Cys Lys Lys His Glu Leu Tyr Val					
				(356)	
1781	1790	1799	1808	1817	
AGC TTC CGG GAT CTG GGA TGG CAG GAC TGG ATT ATA GCA CCA GAA					
Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu					
(362)					
1826	1835	1844	1853	1862	
GGA TAC GCT GCA TTT TAT TGT GAT GGA GAA TGT TCT TTT CCA CTT					
Gly Tyr Ala Ala Phe Tyr Cys Asp Gly Glu Cys Ser Phe Pro Leu					
1871	1880	1889	1898	1907	
AAC GCC CAT ATG AAT GCC ACC AAC CAC GCT ATA GTT CAG ACT CTG					
Asn Ala His MET Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu					
1916	1925	1934	1943	1952	
GTT CAT CTG ATG TTT CCT GAC CAC GTA CCA AAG CCT TGT TGT GCT					
Val His Leu MET Phe Pro Asp His Val Pro Lys Pro Cys Cys Ala					
1961	1970	1979	1988	1997	
CCA ACC AAA TTA AAT GCC ATC TCT GTT CTG TAC TTT GAT GAC AGC					
Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser					
2006	2015	2024	2033	2042	
TCC AAT GTC ATT TTG AAA AAA TAT AGA AAT ATG GTA GTA CGC TCA					
Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn MET Val Val Arg Ser					
				(450)	
2051	2060	2070	2080	2090	2100
TGT GGC TGC CAC TAATATTAAA TAATATTGAT AATAACAAAA AGATCTGTAT					
Cys Gly Cys His					
(454)					
2110	2120	2130	2140	2150	
TAAGGTTTAT GGCTGCAATA AAAAGCATAC TTTCAGACAA ACAGAAAAAA AAA					

The tryptic sequence His-Glu-Leu-Tyr-Val-Ser-Phe-(Ser) described above is noted to be similar to the sequence His-Pro-Leu-Tyr-Val-Asp-Phe-Ser found in the bovine and human cartilage/bone protein BMP-2A sequence, for instance as described in Publication WO 88/00205. Human BMP-5 shares homology with other BMP molecules as well as other members of the TGF- β superfamily of molecules. The cysteine-rich carboxy-terminal 102 amino acid residues of human BMP-5 shares the following homologies with BMP proteins disclosed herein and in Publications WO 88/00205 and WO 89/10409 described above: 61% identity with BMP-2; 43% identity with BMP-3, 59% identity with BMP-4; 91% identity with BMP-6; and 88% identity with BMP-7. Human BMP-5 further shares the following homologies: 38% identity with TGF- β 3; 37% identity with TGF- β 2; 36% identity with TGF- β 1; 25% identity with Mullerian Inhibiting Substance (MIS), a testicular glycoprotein that causes regression of the Mullerian duct during development of the male embryo; 25% identity with inhibin α ; 38% identity with inhibin β_B ; 45% identity with inhibin β_A ; 56% identity with Vgl, a *Xenopus* factor which may be involved in mesoderm induction in early embryogenesis (Weeks and Melton, Cell 51:861-867 (1987)); and 57% identity with Dpp the product of the *Drosophila* decapentaplegic locus which is required for dorsal-ventral specification in early embryogenesis and is involved in various other developmental processes at later stages of development [Padgett, et al., Nature 325:81-84 (1987)].

C. Human BMP-6 Proteins

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Six clones which hybridize to the second probe described in Example V.A. more strongly than to the third are picked and transformed into plasmids. Restriction mapping, Southern blot analysis, and DNA sequence analysis of these plasmids indicate that there are two classes of clones. Clones U2-7 and U2-10 contain human BMP-6 coding sequence based on their stronger hybridization to the second probe and closer DNA homology to the bovine BMP-6 sequence of Table II than the other 4 clones. DNA sequence data derived from these clones indicates that they encode a partial polypeptide of 132 amino acids comprising the carboxy-terminus of the human BMP-6 protein. U2-7 was deposited with the American Type Culture Collection (ATCC), Rockville, Maryland on June 23, 1989 under accession number 68021 under the provisions of the Budapest Treaty.

A primer extended cDNA library is made from U-2 OS mRNA using the oligonucleotide GGAATCCAAGGCAGAATGTG, the sequence being based on the 3' untranslated sequence of the human BMP-6 derived from the clone U2-10. This library is screened with an oligonucleotide of the sequence CAGAGTCGTAATCGC, derived from the BMP-6 coding sequence of U2-7 and U2-10. Hybridization is in standard hybridization buffer (SHB) at 42 degrees centigrade, with wash conditions of 42 degrees centigrade, 5X SSC, 0.1% SDS. Positively hybridizing clones are isolated. The DNA insert of one of these clones, PEH6-2, indicates that it extends further in a 5' direction than either U2-7 or U2-10. A primer extended cDNA library constructed from U-20S mRNA as above is screened with an oligonucleotide of the sequence GCCTCTCCCCCTCCGACGCCCGTCCTCGT, derived from the

sequence near the 5' end of PEH6-2. Hybridization is at 65 degrees centigrade in SHB, with washing at 65 degrees centigrade in 2X SSC, 0.1% SDS. Positively hybridizing recombinants are isolated and analyzed by restriction mapping and DNA sequence analysis.

The 5' sequence of the insert of one of the positively hybridizing recombinants, PE5834#7, is used to design an oligonucleotide of the sequence CTGCTGCTCCTCCTGCTGCCGGAGCGC. A random primed cDNA library [synthesized as for an oligo (dT) primed library except that (dN)₆ is used as the primer] is screened with this oligonucleotide by hybridization at 65 degrees centigrade in SHB with washing at 65 degrees centigrade in 1X SSC, 0.1% SDS. A positively hybridizing clone, RP10, is identified, isolated, and the DNA sequence sequence from the 5' end of its insert is determined. This sequence is used to design an oligonucleotide of the sequence TCGGGCTTCCTGTACCGGCGGCTCAAGACGCAGGAGAAGCGGGAGATGCA. A human placenta cDNA library (Stratagene catalog #936203) is screened with this oligonucleotide by hybridization in SHB at 65 degrees centigrade, and washing at 65 degrees centigrade with 0.2 X SSC, 0.1% SDS. A positively hybridizing recombinant designated BMP6C35 is isolated. DNA sequence analysis of the insert of this recombinant indicates that it encodes the complete human BMP-6 protein. BMP6C35 was deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Maryland USA on March 1, 1990 under Accession Number 68245 under the provisions of the Budapest Treaty.

The DNA and derived amino acid sequence of the

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majority of the insert of BMP6C35 is given in Table IV. This DNA sequence contains an open reading frame of 1539 base pairs which encodes the 513 amino acid human BMP-6 protein precursor. The presumed initiator methionine codon is preceded by a 5'untranslated sequence of 159 base pairs with stop codons in all three reading frames. The stop codon at nucleotides 1699-1701 is followed by at least 1222 base pairs of 3'untranslated sequence. It is noted that U2-7 has a C residue at the position corresponding to the T residue at position 1221 of BMP6C35; U2-7 also has a C residue at the position corresponding to the G residue at position 1253 of BMP6C35. These do not cause amino acid differences in the encoded proteins, and presumably represent allelic variations.

The oligonucleotide TCGGGCTTCCTGTACCGGCGGCTCAAGACGCAGGAGAAGCGGGAGATGCA is used to screen a human genomic library (Toole et al supra), by hybridizing nitrocellulose replicas of 1×10^6 recombinants with the oligonucleotide in SHB at 65 degrees centigrade, and washing at 65 degrees centigrade with 0.2 X SSC, 0.1% SDS. Positively hybridizing clones are purified. The oligonucleotide hybridizing region is localized to an approximately 1.5 kb Pst I fragment. DNA sequence analysis of this fragment confirms the 5' sequence indicated in Table IV.

The first underlined portion of the sequence in Table IV from amino acid #388 to #396, Ser-Thr-Gln-Ser-Gln-Asp-Val-Ala-Arg, corresponds to the similar sequence Ser-Thr-Pro-Alg-Gln-Asp-Val-Ser-Arg of the bovine sequence described above and set forth in Table II. The second underlined sequence

in Table IV from amino acid #415 through #421 His-Glu-Leu-Tyr-Val-Ser-Phe, corresponds to the tryptic fragment identified above from which the oligonucleotide probes are designed. The tryptic sequence His-Glu-Leu-Tyr-Val-Ser-Phe-(Ser) is noted to be similar to a sequence found in other BMP proteins for example the sequence His-Pro-Leu-Tyr-Val-Asp-Phe-Ser found in the bovine and human cartilage/bone protein BMP-2 sequence as described in Publication WO 88/00205. BMP-6 therefore represents a new member of the BMP subfamily of TGF- β like molecules which includes the molecules BMP-2, BMP-3, BMP-4 described in Publications WO 88/00205 and WO 89/10409, as well as BMP-5 and BMP-7 described herein.

Based on knowledge of other BMP proteins, as well as other proteins in the TGF- β family, BMP-6 is predicted to be synthesized as a precursor molecule and the precursor polypeptide would be cleaved between amino acid #381 and amino acid #382 yielding a 132 amino acid mature polypeptide with a calculated molecular weight of approximately 15Kd. The mature form of BMP-6 contains three potential N-linked glycosylation sites per polypeptide chain as does BMP-5.

The processing of BMP-6 into the mature form is expected to involve dimerization and removal of the N-terminal region in a manner analogous to the processing of the related protein TGF- β [L.E. Gentry, et al., (1988); R. Dernyck, et al., (1985) supra]. It is contemplated that the active BMP-6 protein molecule is a dimer. It is further contemplated that the mature active species of BMP-5 comprises protein molecule is a homodimer comprised of two polypeptide subunits each subunit

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comprising amino acid #382 - #513 as set forth in Table IV. Further active species of BMP-5 are contemplated such as phoprotein dimers or a proprotein subunit and a mature subunit.

5 Additional active BMP-5 proteins may comprise amino acid #388 - #513 thereby including the tryptic fragments found in the purified bovine material.

Another BMP-5 protein of the invention comprises amino acid #412 - #513 thereby including the first
10 conserved cystine residue.

TABLE IV

10	20	30	40	50
CGACCATGAG	AGATAAGGAC	TGAGGGCCAG	GAAGGGGAAG	CGAGCCCCGCC
60	70	80	90	100
GAGAGGTGGC	GGGGACTGCT	CACGCCAAGG	GCCACAGCGG	CCGCGCTCCG
110	120	130	140	150
GCCTCGCTCC	GCCGCTCCAC	GCCTCGCGGG	ATCCGCGGGG	GCAGCCCCGGC
159	168	177	186	195
CGGGCGGGG	ATG CCG GGG CTG GGG CGG AGG GCG CAG TGG CTG TGC			
	MET Pro Gly Leu Gly Arg Arg Ala Gln Trp Leu Cys			
(1)				
204	213	222	231	240
TGG TGG TGG GGG CTG CTG TGC AGC TGC TGC GGG CCC CCG CCG CTG				
Trp Trp Trp Gly Leu Leu Cys Ser Cys Cys Gly Pro Pro Pro Leu				
249	258	267	276	285
CGG CCG CCC TTG CCC GCT GCC GCG GCC GCC GCC GCG GGG GGG CAG				
Arg Pro Pro Leu Pro Ala Ala Ala Ala Ala Ala Ala Gly Gly Gln				
294	303	312	321	330
CTG CTG GGG GAC GGC GGG AGC CCC GGC CGC ACG GAG CAG CCG CCG				
Leu Leu Gly Asp Gly Gly Ser Pro Gly Arg Thr Glu Gln Pro Pro				
339	348	357	366	375
CCG TCG CCG CAG TCC TCC TCG GGC TTC CTG TAC CGG CGG CTC AAG				
Pro Ser Pro Gln Ser Ser Ser Gly Phe Leu Tyr Arg Arg Leu Lys				
384	393	402	411	420
ACG CAG GAG AAG CGG GAG ATG CAG AAG GAG ATC TTG TCG GTG CTG				
Thr Gln Glu Lys Arg Glu MET Gln Lys Glu Ile Leu Ser Val Leu				
429	438	447	456	465
GGG CTC CCG CAC CGG CCC CGG CCC CTG CAC GGC CTC CAA CAG CCG				
Gly Leu Pro His Arg Pro Arg Pro Leu His Gly Leu Gln Gln Pro				

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Table IV
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		474			483			492			501			510
CAG	CCC	CCG	GCG	CTC	CGG	CAG	CAG	GAG	GAG	CAG	CAG	CAG	CAG	CAG
Gln	Pro	Pro	Ala	Leu	Arg	Gln	Gln	Glu	Glu	Gln	Gln	Gln	Gln	Gln
		519			528			537			546			555
CAG	CTG	CCT	CGC	GGA	GAG	CCC	CCT	CCC	GGG	CGA	CTG	AAG	TCC	GCG
Gln	Leu	Pro	Arg	Gly	Glu	Pro	Pro	Pro	Gly	Arg	Leu	Lys	Ser	Ala
		564			573			582			591			600
CCC	CTC	TTC	ATG	CTG	GAT	CTG	TAC	AAC	GCC	CTG	TCC	GCC	GAC	AAC
Pro	Leu	Phe	MET	Leu	Asp	Leu	Tyr	Asn	Ala	Leu	Ser	Ala	Asp	Asn
		609			618			627			636			645
GAC	GAG	GAC	GGG	GCG	TCG	GAG	GGG	GAG	AGG	CAG	CAG	TCC	TGG	CCC
Asp	Glu	Asp	Gly	Ala	Ser	Glu	Gly	Glu	Arg	Gln	Gln	Ser	Trp	Pro
		654			663			672			681			690
CAC	GAA	GCA	GCC	AGC	TCG	TCC	CAG	CGT	CGG	CAG	CCG	CCC	CCG	GGC
His	Glu	Ala	Ala	Ser	Ser	Ser	Gln	Arg	Arg	Gln	Pro	Pro	Gly	Ser
		699			708			717			726			735
GCC	GCG	CAC	CCG	CTC	AAC	CGC	AAG	AGC	CTT	CTG	GCC	CCC	GGA	TCT
Pro	Pro	Gly	Ala	Ala	His	Pro	Leu	Asn	Arg	Lys	Ser	Leu	Leu	Ala
		744			753			762			771			780
GGC	AGC	GGC	GGC	GCG	TCC	CCA	CTG	ACC	AGC	GCG	CAG	GAC	AGC	GCC
Gly	Ser	Gly	Gly	Ala	Ser	Pro	Leu	Thr	Ser	Ala	Gln	Asp	Ser	Ala
		789			798			807			816			825
TTC	CTC	AAC	GAC	GCG	GAC	ATG	GTC	ATG	AGC	TTT	GTG	AAC	CTG	GTG
Phe	Leu	Asn	Asp	Ala	Asp	MET	Val	MET	Ser	Phe	Val	Asn	Leu	Val
		834			843			852			861			870
GAG	TAC	GAC	AAG	GAG	TTC	TCC	CCT	CGT	CAG	CGA	CAC	CAC	AAA	GAG
Glu	Tyr	Asp	Lys	Glu	Phe	Ser	Pro	Arg	Gln	Arg	His	His	Lys	Glu
		879			888			897			906			915
TTC	AAG	TTC	AAC	TTA	TCC	CAG	ATT	CCT	GAG	GGT	GAG	GTG	GTG	ACG
Phe	Lys	Phe	Asn	Leu	Ser	Gln	Ile	Pro	Glu	Gly	Glu	Val	Val	Thr

Table IV
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924			933			942			951			960		
GCT	GCA	GAA	TTC	CGC	ATC	TAC	AAG	GAC	TGT	GTT	ATG	GGG	AGT	TTT
Phe	Arg	Ile	Tyr	Lys	Asp	Cys	Val	MET	Ala	Ala	Glu	Gly	Ser	Phe
969			978			987			996			1005		
AAA	AAC	CAA	ACT	TTT	CTT	ATC	AGC	ATT	TAT	CAA	GTC	TTA	CAG	GAG
Lys	Asn	Gln	Thr	Phe	Leu	Ile	Ser	Ile	Tyr	Gln	Val	Leu	Gln	Glu
1014			1023			1032			1041			1050		
CAT	CAG	CAC	AGA	GAC	TCT	GAC	CTG	TTT	TTG	TTG	GAC	ACC	CGT	GTA
His	Gln	His	Arg	Asp	Ser	Asp	Leu	Phe	Leu	Leu	Asp	Thr	Arg	Val
1059			1068			1077			1086			1095		
GTA	TGG	GCC	TCA	GAA	GAA	GGC	TGG	CTG	GAA	TTT	GAC	ATC	ACG	GCC
Val	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Glu	Phe	Asp	Ile	Thr	Ala
1104			1113			1122			1131			1140		
ACT	AGC	AAT	CTG	TGG	GTT	GTG	ACT	CCA	CAG	CAT	AAC	ATG	GGG	CTT
Thr	Ser	Asn	Leu	Trp	Val	Val	Thr	Pro	Gln	His	Asn	MET	Gly	Leu
1149			1158			1167			1176			1185		
CAG	CTG	AGC	GTG	GTG	ACA	AGG	GAT	GGA	GTC	CAC	GTC	CAC	CCC	CGA
Gln	Leu	Ser	Val	Val	Thr	Arg	Asp	Gly	Val	His	Val	His	Pro	Arg
1194			1203			1212			1221			1230		
GCC	GCA	GGC	CTG	GTG	GGC	AGA	GAC	GGC	CCT	TAC	GAT	AAG	CAG	CCC
Ala	Ala	Gly	Leu	Val	Gly	Arg	Asp	Gly	Pro	Tyr	Asp	Lys	Gln	Pro
1239			1248			1257			1266			1275		
TTC	ATG	GTG	GCT	TTC	TTC	AAA	GTG	AGT	GAG	GTC	CAC	GTG	CGC	ACC
Phe	MET	Val	Ala	Phe	Phe	Lys	Val	Ser	Glu	Val	His	Val	Arg	Thr
1284			1293			1302			1311			1320		
ACC	AGG	TCA	GCC	TCC	AGC	CGG	CGC	CGA	CAA	CAG	AGT	CGT	AAT	CGC
Thr	Arg	Ser	Ala	Ser	Ser	Arg	Arg	Arg	Gln	Gln	Ser	Arg	Asn	Arg
1329			1338			1347			1356			1365		
TCT	ACC	CAG	TCC	CAG	GAC	GTG	GCG	CGG	GTC	TCC	AGT	GCT	TCA	GAT
Ser	Thr	Gln	Ser	Gln	Asp	Val	Ala	Arg	Val	Ser	Ser	Ala	Ser	Asp
(388)														

(382)

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Table IV
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1374	1383	1392	1401	1410
TAC AAC AGC AGT GAA TTG AAA ACA GCC TGC AGG AAG CAT GAG CTG				
Tyr Asn Ser Ser Glu Leu Lys Thr Ala Cys Arg Lys <u>His Glu Leu</u>				
		(412)		
1419	1428	1437	1446	1455
TAT GTG AGT TTC CAA GAC CTG GGA TGG CAG GAC TGG ATC ATT GCA				
<u>Tyr Val Ser Phe</u> Gln Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala				
1464	1473	1482	1491	1500
CCC AAG GGC TAT GCT GCC AAT TAC TGT GAT GGA GAA TGC TCC TTC				
Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu Cys Ser Phe				
1509	1518	1527	1536	1545
CCA CTC AAC GCA CAC ATG AAT GCA ACC AAC CAC GCG ATT GTG CAG				
Pro Leu Asn Ala His MET Asn Ala Thr Asn His Ala Ile Val Gln				
1554	1563	1572	1581	1590
ACC TTG GTT CAC CTT ATG AAC CCC GAG TAT GTC CCC AAA CCG TGC				
Thr Leu Val His Leu MET Asn Pro Glu Tyr Val Pro Lys Pro Cys				
1599	1608	1617	1626	1635
TGT GCG CCA ACT AAG CTA AAT GCC ATC TCG GTT CTT TAC TTT GAT				
Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp				
1644	1653	1662	1671	1680
GAC AAC TCC AAT GTC ATT CTG AAA AAA TAC AGG AAT ATG GTT GTA				
Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn MET Val Val				
1689	1698	1708	1718	1728
AGA GCT TGT GGA TGC CAC TAACTCGAAA CCAGATGCTG GGGACACACA				
Arg Ala Cys Gly Cys His				
(513)				
1738	1748	1758	1768	1778
TTCTGCCTTG GATTCTAGA TTACATCTGC CTTAAAAAAA CACGGAAGCA				
1788	1798	1808	1818	1828
CAGTTGGAGG TGGGACGATG AGACTTTGAA ACTATCTCAT GCCAGTGCCT				
1838	1848	1858	1868	1878

Table IV
(page 5 of 6)

TATTACCCAG	GAAGATTTTA	AAGGACCTCA	TTAATAATTT	GCTCACTTGG
1888 TAAATGACGT	1898 GAGTAGTTGT	1908 TGGTCTGTAG	1918 CAAGCTGAGT	1928 TTGGATGTCT
1938 GTAGCATAAG	1948 GTCTGGTAAC	1958 TGCAGAAACA	1968 TAACCGTGAA	1978 GCTCTTCCTA
1988 CCCTCCTCCC	1998 CCAAAAACCC	2008 ACCAAAATTA	2018 GTTTGTAGCTG	2028 TAGATCAAGC
2038 TATTTGGGGT	2048 GTTTGTTAGT	2058 AAATAGGGAA	2068 AATAATCTCA	2078 AAGGAGTTAA
2088 ATGTATTCTT	2098 GGCTAAAGGA	2108 TCAGCTGGTT	2118 CAGTACTGTC	2128 TATCAAAGGT
2138 AGATTTTACA	2148 GAGAACAGAA	2158 ATCGGGGAAG	2168 TGGGGGGAAC	2178 GCCTCTGTTC
2188 AGTTCATTCC	2198 CAGAAGTCCA	2208 CAGGACGCAC	2218 AGCCCAGGCC	2228 ACAGCCAGGG
2238 CTCCACGGGG	2248 CGCCCTTGTC	2258 TCAGTCATTG	2268 CTGTTGTATG	2278 TTCGTGCTGG
2288 AGTTTTGTTG	2298 GTGTGAAAAT	2308 ACACTTATTT	2318 CAGCCAAAAC	2328 ATACCATTTC
2338 TACACCTCAA	2348 TCCTCCATTT	2358 GCTGTACTCT	2368 TTGCTAGTAC	2378 CAAAAGTAGA
2388 CTGATTACAC	2398 TGAGGTGAGG	2408 CTACAAGGGG	2418 TGTGTAACCG	2428 TGTAACACGT
2438 GAAGGCAGTG	2448 CTCACCTCTT	2458 CTTTACCAGA	2468 ACGGTTCTTT	2478 GACCAGCACA

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Table IV
(page 6 of 6)

2488	2498	2508	2518	2528
TTAACTTCTG	GACTGCCGGC	TCTAGTACCT	TTTCAGTAAA	GTGGTTCTCT
2538	2548	2558	2568	2578
GCCTTTTAC	TATACAGCAT	ACCACGCCAC	AGGGTTAGAA	CCAACGAAGA
2588	2598	2608	2618	2628
AAATAAAATG	AGGGTGCCCA	GCTTATAAGA	ATGGTGTTAG	GGGGATGAGC
2638	2648	2658	2668	2678
ATGCTGTTTA	TGAACGGAAA	TCATGATTTC	CCTGTAGAAA	GTGAGGCTCA
2688	2698	2708	2718	2728
GATTAAATTT	TAGAATATTT	TCTAAATGTC	TTTTTCACAA	TCATGTGACT
2738	2748	2758	2768	2778
GGGAAGGCAA	TTTCATACTA	AACTGATTAA	ATAATACATT	TATAATCTAC
2788	2798	2808	2818	2828
AACTGTTTGC	ACTTACAGCT	TTTTTTGTAA	ATATAAACTA	TAATTTATTG
2838	2848	2858	2868	2878
TCTATTTTAT	ATCTGTTTTG	CTGTGGCGTT	GGGGGGGGGG	CCGGGCTTTT
2888	2898	2908	2918	
GGGGGGGGGG	GTTTGTTTGG	GGGGTGTCGT	GGTGTGGGCG	GGCGG

Comparison of the sequence of murine Vgr-1 [Lyons, et al., PNAS 86:4554 (1989)] to human BMP-6 reveals a degree of amino acid sequence identity greater than 92%. The murine Vgr-1 is likely the murine homologue of BMP-6. Human BMP-6 shares homology with other BMP molecules as well as other members of the TGF- β superfamily of molecules. The cysteine-rich carboxy-terminal 102 amino acid residues of human BMP-6 shares the following homologies with BMP proteins disclosed herein and in Publications WO 88/00205 and WO 89/10409: 61% identity with BMP-2; 44% identity with BMP-3, 60% identity with BMP-4; 91% identity with BMP-5; and 87% identity with BMP-7. Human BMP-6 further shares the following homologies: 41% identity with TGF- β 3; 39% identity with TGF- β 2; 37% identity with TGF- β 1; 26% identity with Mullerian Inhibiting Substance (MIS), a testicular glycoprotein that causes regression of the Mullerian duct during development of the male embryo; 25% identity with inhibin α ; 43% identity with inhibin β_B ; 49% identity with inhibin β_A ; 58% identity with Vgl, a Xenopus factor which may be involved in mesoderm induction in early embryogenesis (Weeks and Melton, (1987) Supra); and 59% identity with Dpp the product of the Drosophila decapentaplegic locus which is required for dorsal-ventral specification in early embryogenesis and is involved in various other developmental processes at later stages of development [Padgett, et al., (1987) supra].

D. Human BMP-7 Proteins

The other four clones of Example V.C. above which appear to represent a second class of clones

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5 encode a novel polypeptide which we designate as
BMP-7. One of these clones, U2-5, was deposited
with the ATCC on June 22, 1989 under accession
number ATCC 68020 under the provisions of the
10 Budapest Treaty. This clone was determined not to
contain the entire coding sequence for BMP-7. An
oligo of the sequence GCGAGCAATGGAGGATCCAG (designed
on the basis of the 3' noncoding sequence of U2-5)
was used to make a primer-extended cDNA library
from U-2 OS mRNA (Toole, et al.). 500,000
15 recombinants of this library were screened with the
oligonucleotide GATCTCGCGCTGCAT (designed on the
basis of the BMP-7 coding sequence) by
hybridization in SHB at 42° and washing in 5X SSC,
0.1% SDS at 42°. Several hybridizing clones were
20 obtained. DNA sequence analysis and derived amino
acid sequence of one of these clones, PEH7-9, is
given in Table V. PEH7-9 was deposited with the
American Type Culture Collection (ATCC), Rockville,
Maryland on November 17, 1989 under accession
number ATCC 68182 under the provisions of the
Budapest Treaty. PEH7-9 contains an insert of 1448
base pairs. This clone, PEH7-9, is expected to
5 contain all of the nucleotide sequence necessary to
encode BMP-7 proteins. The cDNA sequence of Table
V contains an open reading frame of 1292 base
pairs, encoding a protein of 431 amino acids,
preceded by a 5' untranslated region of 96 base
pairs with stop codons in all frames, and contains
10 a 3' untranslated region of 60 base pairs following
the in frame stop codon TAG.

This protein of 431 amino acids has a
molecular weight of 49,000 daltons as predicted by
its amino acid sequence and is contemplated to
3 represent the primary translation product. Based

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on knowledge of other BMP proteins as well as other proteins within the TGF- β family, it is predicted that the precursor polypeptide would be cleaved between amino acid #299 and #300, yielding a 132 amino acid mature peptide.

It is contemplated that processing of BMP-7 to the mature form involves dimerization of the proprotein and removal of the N-terminal region in a manner analogous to the processing of the related protein TGF- β [L.E. Gentry, et al., (1988) Supra and; R. Dernyck, et al., (1985) Supra]. It is contemplated therefore that the mature active species of BMP-7 comprises a homodimer of 2 polypeptide subunits each subunit comprising amino acid #300 - #431 as shown in Table V with a calculated weight of 15,000 daltons. Other active BMP-7 species are contemplated, for example, protein dimers or proprotein subunits linked to mature subunits. Additional active species may comprise amino acids #309 - #431 of Table V such species including the tryptic sequences found in the purified bovine material. Also contemplated are BMP-7 proteins comprising amino acids #330-#431 thereby including the first conserved cysteine residue.

The underlined sequence of Table V from amino acid #309 - #314 Asn-Gln-Glu-Ala-Leu-Arg is the same sequence as that of tryptic fragment #5 found in the 28,000 - 30,000 dalton purified bone preparation as described in the "BMP" Publications WO 88/00205 and WO 89/10409 mentioned above. The underlined sequence of Table V from amino acid #333-#339 His-Glu-Leu-Tyr-Val-Ser-Phe corresponds to the tryptic fragment identified in the bovine bone preparation described above from which the

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oligonucleotide probes are designed.

TABLE V

10	20	30	40	50
GTGACCGAGC	GGGOGGGAAG	GGGGGCTGGC	CCCTCTGGCA	CGTGGGGGGG
60	70	80	90	99
TGOGGGGCGG	GAGCGGGGAG	CGGGGGTAGC	GCGTAGAGGC	GGGCGG
				ATG
				MET
				(1)
108	117	126	135	144
CAC GTG CGC TCA CTG CGA GGT GCG GCG CCG CAC AGC TTC GTG GCG				
His Val Arg Ser Leu Arg Ala Ala Pro His Ser Phe Val Ala				
153	162	171	180	189
CTC TGG GCA CCC CTG TTC CTG CTG GCG TOC GCG CTG GCG GAC TTC				
Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe				
198	207	216	225	234
AGC CTG GAC AAC GAG GTG CAC TCG AGC TTC ATC CAC CGG GCG CTC				
Ser Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu				
243	252	261	270	279
CGC AGC CAG GAG CGG CGG GAG ATG CAG GCG GAG ATC CTC TOC ATT				
Arg Ser Gln Glu Arg Arg Glu MET Gln Arg Glu Ile Leu Ser Ile				
288	297	306	315	324
TTG GGC TTG CCC CAC CGC CGG CGC CGG CAC CTC CAG GGC AAG CAC				
Leu Gly Leu Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His				
333	342	351	360	369
AAC TCG GCA CCC ATG TTC ATG CTG GAC CTG TAC AAC GCG ATG GCG				
Asn Ser Ala Pro MET Phe MET Leu Asp Leu Tyr Asn Ala MET Ala				
378	387	396	405	414
GTG GAG GAG GGC GGC GGG CCC GGC GGC CAG GGC TTC TOC TAC CCC				
Val Glu Glu Gly Gly Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro				
423	432	441	450	459
TAC AAG GCG GTC TTC AGT ACC CAG GGC CCC CCT CTG GCG AGC CTG				
Tyr Lys Ala Val Phe Ser Thr Gln Gly Pro Pro Leu Ala Ser Leu				
468	477	486	495	504
CAA GAT AGC CAT TTC CTC ACC GAC GCG GAC ATG GTC ATG AGC TTC				
Gln Asp Ser His Phe Leu Thr Asp Ala Asp MET Val MET Ser Phe				
513	522	531	540	549
GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC CAC CCA GCG TAC				
Val Asn Leu Val Glu His Asp Lys Glu Phe Phe His Pro Arg Tyr				

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Table V
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558	567	576	585	594
CAC CAT CGA GAG TTC CGG TTT GAT CTT TOC AAG ATC CCA GAA GGG				
His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile Pro Glu Gly				
603	612	621	630	639
GAA GCT GTC ACG GCA GGC GAA TTC CGG ATC TAC AAG GAC TAC ATC				
Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp Tyr Ile				
648	657	666	675	684
CGG GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT CAG				
Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr Gln				
693	702	711	720	729
GTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC				
Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu				
738	747	756	765	774
GAC AGC CGT ACC CTC TGG GGC TCG GAG GAG GGC TGG CTG GTG TTT				
Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe				
783	792	801	810	819
GAC ATC ACA GGC ACC AGC AAC CAC TGG GTG GTC AAT CCG CCG CAC				
Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His				
828	837	846	855	864
AAC CTG GGC CTG CAG CTC TCG GTG GAG ACG CTG GAT GGG CAG AGC				
Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser				
873	882	891	900	909
ATC AAC CCC AAG TTG GCG GGC CTG ATT GGG CCG CAC GGG CCC CAG				
Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln				
918	927	936	945	954
AAC AAG CAG CCC TTC ATG GTG GCT TTC TTC AAG GGC ACG GAG GTC				
Asn Lys Gln Pro Phe MET Val Ala Phe Phe Lys Ala Thr Glu Val				
963	972	981	990	999
CAC TTC CGC AGC ATC CGG TOC ACG GGG AGC AAA CAG CCG AGC CAG				
His Phe Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln				
1008	1017	1026	1035	1044
AAC CGC TOC AAG ACG CCC AAG AAC CAG GAA GGC CTG CCG ATG GGC				
Asn Arg Ser Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg MET Ala				
1053	1062	1071	1080	1089
AAC GTG GCA GAG AAC AGC AGC AGC AGC CAG AGG CAG GGC TGT AAG				
Asn Val Ala Glu Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys				

(300)

(309)

(330)

Table V
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1098	1107	1116	1125	1134
AAG CAC GAG CTG TAT GTC AGC TTC CGA GAC CTG GGC TGG CAG GAC				
Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln Asp				
1143	1152	1161	1170	1179
TGG ATC ATC GCG CCT GAA GGC TAC GGC GGC TAC TAC TGT GAG GGG				
Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly				
1188	1197	1206	1215	1224
GAG TGT GGC TTC CCT CTG AAC TCC TAC ATG AAC GGC ACC AAC CAC				
Glu Cys Ala Phe Pro Leu Asn Ser Tyr MET Asn Ala Thr Asn His				
1233	1242	1251	1260	1269
GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC CCG GAA ACG GTG				
Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Ile Ser Val				
1278	1287	1296	1305	1314
CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GGC ATC TCC GTC				
Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser Val				
1323	1332	1341	1350	1359
CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA TAC AGA				
Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg				
1368	1377	1386	1399	
AAC ATG GTG GTC CCG GGC TGT GGC TGC CAC TAGCTCTCTCC				
Asn MET Val Val Arg Ala Cys Gly Cys His				
		(431)		
1409	1419	1429	1439	1448
GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTTGCTC				

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Like BMP-5 and BMP-6, human BMP-7 shares homology with other BMP molecules as well as other members of the TGF- β superfamily of molecules. The cysteine-rich carboxy-terminal 102 amino acids residues of human BMP-7 shares the following homologies with BMP proteins herein and in Publications WO 88/00205 and WO 89/10409 described above: 60% identity with BMP-2; 43% identity with BMP-3, 58% identity with BMP-4, 87% identity with BMP-6; and 88% identity with BMP-5. Human BMP-7 further shares the following homologies: 40% identity with TGF- β 3; 40% identity with TGF- β 2; 36% identity with TGF- β 1; 29% identity with Mullerian Inhibiting Substance (MIS), a testicular glycoprotein that causes regression of the Mullerian duct during development of the male embryo; 25% identity with inhibin- α ; 44% identity with inhibin- β B; 45% identity with inhibin- β A; 57% identity with Vgl, a *Xenopus* factor which may be involved in mesoderm induction in early embryogenesis [Weeks and Melton, (1987) Supra.]; and 58% identity with Dpp the product of the *Drosophila* decapentaplegic locus which is required for dorsal-ventral specification in early embryogenesis and is involved in various other developmental processes at later stages of development [Padgett, et al., (1987) Supra.].

The invention encompasses the genomic sequences of BMP-5, BMP-6 and BMP-7. To obtain these sequences the cDNA sequences described herein are utilized as probes to screen genomic libraries using techniques known to those skilled in the art.

The procedures described above and additional

methods known to those skilled in the art may be employed to isolate other related proteins of interest by utilizing the bovine or human proteins as a probe source. Such other proteins may find similar utility in, inter alia, fracture repair, wound healing and tissue repair.

EXAMPLE VI

Expression of BMP Proteins

In order to produce bovine, human or other mammalian BMP-5, BMP-6 or BMP-7 proteins of the invention, the DNA encoding it is transfected into an appropriate expression vector and introduced into mammalian cells or other preferred eukaryotic or prokaryotic hosts by conventional genetic engineering techniques. It is contemplated that the preferred expression system for biologically active recombinant human proteins of the invention will be stably transformed mammalian cells. For transient expression, the cell line of choice is SV40 transformed African green monkey kidney COS-1 or COS-7 which typically produce moderate amounts of the protein encoded within the plasmid for a period of 1-4 days. For stable high level expression of BMP-5, BMP-6 or BMP-7 the preferred cell line is Chinese hamster Ovary (CHO). It is therefore contemplated that the preferred mammalian cells will be CHO cells.

The transformed host cells are cultured and the BMP proteins of the invention expressed thereby are recovered, isolated and purified. Characterization of expressed proteins is carried out using standard techniques. For example, characterization may include pulse labeling with [³⁵S] methionine or cysteine and analysis by

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polyacrylamide electrophoresis. The recombinantly expressed BMP proteins are free of proteinaceous materials with which they are co-produced and with which they ordinarily are associated in nature, as well as from other contaminants, such as materials found in the culture media.

A. Vector Construction

As described above, numerous expression vectors known in the art may be utilized in the expression of BMP proteins of the invention. The vector utilized in the following examples is pMT21, a derivative of pMT₂, though other vectors may be suitable in practice of the invention.

pMT₂ is derived from pMT2-VWF, which has been deposited with the American Type Culture Collection (ATCC), Rockville, MD (USA) under accession number ATCC 67122 under the provisions of the Budapest Treaty. EcoRI digestion excises the cDNA insert present in pMT-VWF, yielding pMT2 in linear form which can be ligated and used to transform E. Coli HB 101 or DH-5 to ampicillin resistance. Plasmid pMT2 DNA can be prepared by conventional methods.

pMT21 is then constructed using loopout/in mutagenesis [Morinaga, et al., Biotechnology 84:636 (1984)]. This removes bases 1075 to 1170 (inclusive). In addition it inserts the following sequence: 5' TCGA 3'. This sequence completes a new restriction site, XhoI. This plasmid now contains 3 unique cloning sites PstI, EcoRI, and XhoI.

In addition, pMT21 is digested with EcoRV and XhoI, treating the digested DNA with Klenow fragment of DNA polymerase I and ligating ClaI linkers (NEBio Labs, CATCGATG). This removes bases

2171 to 2420 starting from the HindIII site near the SV40 origin of replication and enhancer sequences of pMT2 and introduces a unique Cla I site, but leaves the adenovirus VAI gene intact.

5

B. BMP-5 Vector Construction

10 A derivative of the BMP-5 cDNA sequence set forth in Table III comprising the the nucleotide sequence from nucleotide #699 to #2070 is specifically amplified. The oligonucleotides CGACCTGGAGCCACCATGCATCTGACTGTA and TGCCTGCAGTTTAATATTAGTGGCAGC are utilized as primers to allow the amplification of nucleotide sequence #699 to #2070 of Table III from the insert of clone 15 U2-16 described above in Example V. This procedure introduces the nucleotide sequence CGACCTGCAGCCACC immediately preceeding nucleotide #699 and the nucleotide sequence CTGCAGGCA immediately following nucleotide #2070. The addition of these sequences results in the creation of PstI restriction 20 endonuclease recognition sites at both ends of the amplified DNA fragment. The resulting amplified DNA product of this procedure is digested with the restriction endonuclease PstI and subcloned into 25 the PstI site of the pMT2 derivative pMT21 described above. The resulting clone is designated H5/5/pMT.

30 The insert of H5/5/pMT is excised by PstI digestion and subcloned into the plasmid vector pSP65 at the PstI site resulting in BMP5/SP6. BMP5/SP6 and U2-16 are digested with the restriction endonucleases NsiI and NdeI to excise the portion of their inserts corresponding to nucleotides #704 to #1876 of Table III. The 35 resulting 1173 nucleotide NsiI-NdeI fragment of

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clone U2-16 is ligated into the NsiI-NdeI site of BMP5/SP6 from which the corresponding 1173 nucleotide NsiI-NdeI fragment had been removed. The resulting clone is designated BMP5mix/SP64.

5 Direct DNA sequence analysis of BMP5mix/SP64 is performed to confirm identity of the nucleotide sequences produced by the amplification to those set forth in Table III. The clone BMP5mix/SP64 is
10 digested with the restriction endonuclease PstI resulting in the excision of an insert comprising the nucleotides #699 to #2070 of Table III and the additional sequences containing the PstI recognition sites as described above. The
15 resulting 1382 nucleotide PstI fragment is subcloned into the PstI site of the pMT2 derivative pMT21. This clone is designated BMP5mix/pMT21#2.

C. BMP-6 Vector Construction

20 A derivative of the BMP-6 cDNA sequence set forth in Table IV comprising the nucleotide sequence from nucleotide #160 to #1706 is produced by a series of techniques known to those skilled in the art. The clone BMP6C35 described above in
25 Example V is digested with the restriction endonucleases ApaI and TaqI, resulting in the excision of a 1476 nucleotide portion of the insert comprising nucleotide #231 to #1703 of the sequence set forth in Table IV. Synthetic oligonucleotides
30 with SalI restriction endonuclease site converters are designed to replace those nucleotides corresponding to #160 to #230 and #1704 to #1706 which are not contained in the 1476 ApaI-TaqI fragment of the BMP-6 cDNA sequence. Oligonucleotide/SalI converters conceived to
35 r e p l a c e t h e m i s s i n g 5 '

(TCGACCCACCATGCCGGGGCTGGGGCGGAGGGCGCAGTGGCTGTG
CTGGTGGT GGGGGCTGTGCTGCAGCTGCTGCGGGCC and
CGCAGCAGCTGCACAGCAGCCCCCACCACCAGCACAGCCACTGCGCC
CTCCGCCCCAG CCCCGGCATGGTGGG) and 3' (TCGACTGGTTT
and CGAAACCAG) sequences are annealed to each other
independently. The annealed 5' and 3' converters
are then ligated to the 1476 nucleotide ApaI-TaqI
described above, creating a 1563 nucleotide
fragment comprising the nucleotide sequence from
#160 to #1706 of Table IV and the additional
sequences contrived to create SalI restriction
endonuclease sites at both ends. The resulting
1563 nucleotide fragment is subcloned into the SalI
site of pSP64. This clone is designated
BMP6/SP64#15.

DNA sequence analysis of BMP6/SP64#15 is
performed to confirm identity of the 5' and 3'
sequences replaced by the converters to the
sequence set forth in Table IV. The insert of
BMP6/SP64#15 is excised by digestion with the
restriction endonuclease SalI. The resulting 1563
nucleotide SalI fragment is subcloned into the XhoI
restriction endonuclease site of the pMT2
derivative pMT21 and designated herein as
BMP6/pMT21.

D. BMP-7 Vector Construction

A derivative of the BMP-7 sequence set forth
in Table V comprising the nucleotide sequence from
nucleotide #97 to #1402 is specifically amplified.
The oligonucleotides CAGGTCGACCCACCATGCACGTGCGCTCA
and TCTGTCGACCTCGGAGGAGCTAGTGGC are utilized as
primers to allow the amplification of nucleotide
sequence #97 to #1402 of Table V from the insert of
clone PEH7-9 described above. This procedure

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generates the insertion of the nucleotide sequence CAGGTCGACCCACC immediately preceeding nucleotide #97 and the insertion of the nucleotide sequence GTCGACAGA immediately following nucleotide #1402.

5 The addition of these sequences results in the creation of a Sall restriction endonuclease recognition site at each end of the amplified DNA fragment. The resulting amplified DNA product of this procedure is digested with the restriction
10 endonuclease Sall and subcloned into the Sall site of the plasmid vector pSP64 resulting in BMP7/SP6#2.

The clones BMP7/SP6#2 and PEH7-9 are digested with the restriction endonucleases NcoI And StuI to
15 excise the portion of their inserts corresponding to nucleotides #363 to #1081 of Table V. The resulting 719 nucleotide NcoI-StuI fragment of clone PEH7-9 is ligated into the NcoI-StuI site of BMP7/SP6#2 from which the corresponding 719
20 nucleotide fragment is removed. The resulting clone is designated BMP7mix/SP6.

Direct DNA sequence analysis of BMP7mix/SP6 confirmed identity of the 3' region to the nucleotide sequence from #1082 to #1402 of Table V,
25 however the 5' region contained one nucleotide misincorporation.

Amplification of the nucleotide sequence (#97 to #1402 of Table V) utilizing PEH7-9 as a template is repeated as described above. The resulting
30 amplified DNA product of this procedure is digested with the restriction endonucleases Sall and PstI. This digestion results in the excision of a 747 nucleotide fragment comprising nucleotide #97 to #833 of Table V plus the additional sequences of
35 the 5' priming oligonucleotide used to create the

SalI restriction endonuclease recognition site described earlier. This 747 SalI-PstI fragment is subcloned into a SalI-PstI digested pSP65 vector resulting in 5'BMP7/SP65. DNA sequence analysis demonstrates that the insert of the 5'BMP7/SP65#1 comprises a sequence identical to nucleotide #97 to #362 of Table V.

The clones BMP7mix/SP6 and 5'BMP7/SP65 are digested with the restriction endonucleases SalI and NcoI. The resulting 3' NcoI-SalI fragment of BMP7mix/SP6 comprising nucleotides #363 to #1402 of Table V and 5' SalI-NcoI fragment of 5'BMP7/SP65 comprising nucleotides #97 to #362 of Table V are ligated together at the NcoI restriction sites to produce a 1317 nucleotide fragment comprising nucleotides #97 to #1402 of Table V plus the additional sequences derived from the 5' and 3' oligonucleotide primers which allows the creation of SalI restriction sites at both ends of this fragment. This 1317 nucleotide SalI fragment is ligated into the SalI site of the pMT2 derivative pMT2Cla-2. This clone is designated BMP7/pMT2.

The insert of BMP7/pMT2 is excised by digestion with the restriction endonuclease SalI. The resulting 1317 nucleotide SalI fragment is subcloned into the SalI restriction site of the vector pSP64. This clone is designated BMP7/SP64#2d. The insert of BMP7/SP64#2d is excised by digestion with SalI and the resulting SalI fragment comprising nucleotides #97 to #1402 of Table V is subcloned into the XhoI restriction endonuclease site of the pMT2 derivative pMT21 described above.

Example VII

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Transient COS Cell Expression

To obtain transient expression of BMP-5, BMP-6, and BMP-7 proteins one of the vectors containing the cDNA for BMP-5, BMP-6 or BMP-7, BMP5mix/pMT21#2, BMP6/pMT21#2, or BMP7/pMT21 respectively, are transfected into COS-1 cells using the electroporation method. Other suitable transfection methods include DEAE-dextran, and lipofection. Approximately 48 hours later, cells are analysed for expression of both intracellular and secreted BMP-5, BMP-6 or BMP-7 protein by metabolic labelling with [³⁵S] methionine and polyacrylamide gel electrophoresis. Intracellular BMP is analyzed in cells which are treated with tunicamycin, an inhibitor of N-linked glycosylation. In tunicamycin-treated cells, the nonglycosylated primary translation product migrates as a homogeneous band of predictable size and is often easier to discern in polyacrylamide gels than the glycosylated form of the protein. In each case, intracellular protein in tunicamycin-treated cells is compared to a duplicate plate of transfected, but untreated COS-1 cells.

A. BMP-5 COS Expression

The results demonstrate that intracellular forms of BMP-5 of approximately 52 Kd and 57 Kd are made by COS cells. The 52 Kd protein is the size predicted by the primary sequence of the the BMP-5 cDNA clone. Following treatment of the cells with tunicamycin, only the 52 Kd form of BMP-5 is made, suggesting that the 57 Kd protein is a glycosylated derivative of the 52 Kd primary translation product. The 57 Kd protein is secreted into the conditioned medium and is apparently not

efficiently processed by COS-1 cells into the pro and mature peptides.

B. BMP-6 COS Expression

5 Intracellular BMP-6 exists as a doublet of approximately 61 Kd and 65 Kd in untreated COS-1 cells. In the presence of tunicamycin, only the 61 Kd protein is observed, indicating that the 65 Kd protein is the glycosylated derivative of the 61 Kd primary translation product. This is similar to
10 the molecular weight predicted by the cDNA clone for BMP-6. In the absence of tunicamycin, the predominant protein secreted from COS-1 cells is the 65 Kd glycosylated, unprocessed clipped form of
15 BMP-6. There are also peptides of 46 Kd and 20 Kd present at lower abundance than the 65 Kd that likely represent the processed pro and mature peptides, respectively.

C. BMP-7 COS Expression

20 Intracellular BMP-7 protein in tunicamycin-treated COS-1 cells is detected as a doublet of 44 Kd and 46 Kd. In the absence of tunicamycin, proteins of 46 Kd and perhaps 48 Kd are synthesized. These likely represent glycosylated
25 derivatives of the BMP-7 primary translation products. The 48 Kd protein is the major BMP species secreted from COS-1 cells, again suggesting inefficient cleavage of BMP-7 at the propeptide dibasic cleavage site.

Example VIII

CHO Cell Expression

35 DHFR deficient CHO cells (DUKX B11) are transfected by electroporation with one of the BMP-5, BMP-6 or BMP-7 expression vectors, described

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above, and selected for expression of DHFR by growth in nucleoside-free media. Other methods of transfection, including but not limited to CaPO_4 precipitation, protoplast fusion, microinjection, and lipofection, may also be employed. In order to obtain higher levels of expression more expediently, cells may be selected in nucleoside-free media supplemented with 5 nM, 20 nM or 100 nM MTX. Since the DHFR selectable marker is physically linked to the BMP cDNA as the second gene of a bicistronic coding region, cells which express DHFR should also express the BMP encoded within the upstream cistron. Either single clones, or pools of combined clones, are expanded and analyzed for expression of BMP protein. Cells are selected in stepwise increasing concentrations of MTX (5 nM, 20 nM, 100 nM, 500 nM, 2 μM , 10 μM , and 100 μM) in order to obtain cell lines which contain multiple copies of the expression vector DNA by virtue of gene amplification, and hence secrete large amounts of BMP protein.

Using standard techniques cell lines are screened for expression of BMP RNA, protein or activity, and high expressing cell lines are cloned or recloned at the appropriate level of selection to obtain a more homogeneous population of cells. The resultant cell line is then further characterized for BMP DNA sequences, and expression of BMP RNA and protein. Suitable cell lines can then be used for producing recombinant BMP protein.

A. CHO Expression of BMP-5

The BMP-5 vector BMP5mix/pMT21#2 described above is transfected into CHO cells by electroporation, and cells are selected for

expression of DHFR. Clonal cell lines are obtained from individual colonies selected stepwise for resistance to MTX, and analyzed for secretion of BMP-5 proteins. In some cases cell lines may be maintained as pools and cloned at later stages of MTX selection.

As described in Example V.B. the cDNA for BMP-5 encodes for a protein of approximately 52 Kd. Following processing within the cell that includes, but may not be limited to, propeptide cleavage, glycosylation, and dimer or multimer formation, multiple BMP-5 peptides are produced. There are at least 4 candidate peptides for processed forms of the BMP-5 protein discernable following SDS PAGE under reducing conditions; a 65 Kd peptide, a 35 Kd peptide, and a doublet of approximately 22 Kd molecular weight. Other less abundant BMP-5 peptides may also be present. By comparison to the processing of other related BMP molecules and the related protein TGF-beta, the 65 Kd protein likely represents unprocessed BMP-5, the 35 Kd species represents the propeptide, and the 22 Kd doublet represents the mature peptide.

Material from a BMP-5 cell line is analyzed in a 2-dimensional gel system. In the first dimension, proteins are electrophoresed under nonreducing conditions. The material is then reduced, and electrophoresed in a second polyacrylamide gel. Proteins that form disulfide-bonded dimers or multimers will run below a diagonal across the second reduced gel. Results from analysis of BMP-5 protein indicates that a significant amount of the mature BMP-5 peptides can form homodimers of approximately 30-35 Kd that reduce to the 22 Kd doublet observed in one

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dimensional reduced gels. A fraction of the mature peptides are apparently in a disulfide-bonded complex with the pro peptide. The amount of this complex is minor relative to the mature homodimer. In addition, some of the unprocessed protein can apparently form homodimers or homomultimers.

B. CHO Expression of BMP-6

The BMP-6 expression vector BMP6/pMT21 described above is transferred into CHO cells and selected for stable transformants via DHFR expression in a manner as described above in part A with relation to BMP-5. The mature active species of BMP-6 is contemplated to comprise amino acid #382 - #513 of Table IV. It is contemplated that secreted BMP-6 protein will be processed in a manner similar to that described above for BMP-5, other related BMP molecules and analogous to the processing of the related protein TGF- β [Gentry, et al.; Dernyck, et al., Supra.].

C. CHO Expression of BMP-7

The BMP-7 expression vector BMP7/pMT21 described above is transfected into CHO cells and selected for stable transformants via DHFR expression in a manner as described above in relation to BMP-5. The mature active species of BMP-7 is contemplated to comprise amino acid #300-#431 of Table V. It is contemplated that secreted BMP-7 protein will be processed in a manner similar to that described above for BMP-5, other related BMP molecules and analogous to the processing of the related protein TGF- β [Gentry, et al.; Dernyck, et al., Supra.].

EXAMPLE IX

Biological Activity of Expressed BMP Proteins

To measure the biological activity of the expressed BMP-5, BMP-6 and BMP-7 proteins obtained in Example VII and VIII above, the BMP proteins are recovered from the culture media and purified by isolating the BMP proteins from other proteinaceous materials with which they are co-produced, as well as from other contaminants. The proteins may be partially purified on a Heparin Sepharose column and further purified using standard purification techniques known to those skilled in the art.

For instance, post transfection conditioned medium supernatant collected from the cultures is concentrated approximately 10 fold by ultrafiltration on a YM 10 membrane and then dialyzed against 20mM Tris, 0.15 M NaCl, pH 7.4 (starting buffer). This material is then applied to a Heparin Sepharose column in starting buffer. Unbound proteins are removed by a wash of starting buffer, and bound proteins, including proteins of the invention, are desorbed by a wash of 20 mM Tris, 2.0 M NaCl, pH 7.4. The proteins bound by the Heparin column are concentrated approximately 10-fold on, for example, a Centricon 10 and the salt reduced by diafiltration with, for example, 0.1% trifluoroacetic acid. The appropriate amount of the resultant solution is mixed with 20 mg of rat matrix and then assayed for in vivo bone and/or cartilage formation activity by the Rosen-modified Sampath - Reddi assay. A mock transfection supernatant fractionation is used as a control.

Further purification may be achieved by

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preparative NaDodSO₄/PAGE [Laemmli, Nature 227:680-685 (1970)]. for instance, approximately 300 µg of protein is applied to a 1.5-mm-thick 12.5% gel: recovery is be estimated by adding L-[³⁵S]methionine-labeled BMP protein purified over heparin-Sepharose as described above. Protein may be visualized by copper staining of an adjacent lane [Lee, et al., Anal. Biochem. 166:308-312 (1987)]. Appropriate bands are excised and extracted in 0.1% NaDodSO₄/20 mM Tris, pH 8.0. The supernatant may be acidified with 10% CF₃COOH to pH 3 and the proteins are desalted on 5.0 x 0.46 cm Vydac C₄ column (The Separations Group, Hesperia, CA) developed with a gradient of 0.1% CF₃COOH to 90% acetonitrile/0.1% CF₃COOH.

The implants containing rat matrix to which specific amounts of human BMP-5, BMP-6 or BMP-7 proteins of the invention have been added are removed from rats after approximately seven days and processed for histological evaluation. Representative sections from each implant are stained for the presence of new bone mineral with von Kossa and acid fuchsin, and for the presence of cartilage-specific matrix formation using toluidine blue. The types of cells present within the section, as well as the extent to which these cells display phenotype are evaluated and scored as described in Example III.

Levels of activity may also be tested for host cell extracts. Purification is accomplished in a similar manner as described above except that 6 M urea is included in all the buffers.

The foregoing descriptions detail presently preferred

embodiments of the present invention. Numerous

modifications and variations in practice thereof are expected to occur to those skilled in the art upon consideration of these descriptions. Those modifications and variations are believed to be encompassed within the claims appended hereto.

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What is claimed is:

1. A purified human BMP protein selected from the group consisting of:
 - (a) BMP-5 characterized by the amino acid sequence comprising amino acid #323 to #454 of Table III;
 - (b) BMP-6 characterized by the amino acid sequence comprising amino acid #382 to #513 of Table IV; and
 - (c) BMP-7 characterized by the amino acid sequence comprising amino acid #300 to #431 of Table V.
2. A purified human BMP protein selected from the group consisting of
 - (a) BMP-5 protein produced by the steps of
 - (i) culturing a cell transformed with a DNA sequence comprising nucleotide #1665 to #2060 of Table III or a sequence substantially homologous thereto; and
 - (ii) recovering, isolating and purifying from said culture medium a protein comprising amino acid #323 to #454 as shown in Table III or a sequence substantially homologous thereto;
 - (b) BMP-6 produced by the steps of
 - (i) culturing a cell transformed with a DNA sequence comprising nucleotide #1303 to #1698 of Table IV or a sequence substantially homologous thereto; and
 - (ii) recovering, isolating and purifying

from said culture medium a protein comprising amino acid #382 to #513 as shown in Table IV or a sequence substantially homologous thereto; and

- (c) BMP-7 protein produced by the steps of
 - (i) culturing a cell transformed with a DNA sequence comprising nucleotide #994 to #1389 of Table V or a sequence substantially homologous thereto; and
 - (ii) recovering, isolating and purifying from said culture medium a protein comprising the amino acid #300 to amino acid #431 as shown in Table V or a sequence substantially homologous thereto.
- 3. A purified human BMP protein selected from the group consisting of
 - (a) BMP-5 produced by the steps of
 - (i) culturing a cell transformed with a DNA sequence comprising nucleotide #699 to #2060 of Table III or a sequence substantially homologous thereto; and
 - (ii) recovering, isolating and purifying from said culture medium said BMP-5 protein;
 - (b) BMP-6 produced by the steps of
 - (i) culturing a cell transformed with a DNA sequence comprising nucleotide #160 to #1698 of Table IV or a sequence substantially homologous thereto; and

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- (ii) recovering, isolating and purifying from said culture medium said BMP-6 protein; and
 - (c) BMP-7 produced by the steps of
 - (i) culturing a cell transformed with a DNA sequence comprising nucleotide #97 to #1389 of Table V or a sequence substantially homologous thereto; and
 - (ii) recovering, isolating and purifying from said culture medium said BMP-7 protein.
4. A purified BMP protein produced by the steps of:
- (a) culturing a cell transformed with a DNA sequence comprising a sequence which hybridizes to the DNA sequence selected from the DNA sequences of Table III comprising nucleotide #1665 - #2060, Table IV comprising nucleotide #1303-#1698 or Table V comprising nucleotide #994 - #1389 under stringent hybridization conditions; and
 - (b) recovering, isolating and purifying from said culture medium a protein characterized by the ability to induce cartilage and/or bone formation.
5. A protein of claim 1 further characterized by the ability to demonstrate the induction of cartilage and/or bone formation.
6. A protein of claim 2 further characterized by the ability to demonstrate the induction of

cartilage and/or bone formation.

7. A protein of claim 3 further characterized by the ability to demonstrate the induction of cartilage and/or bone formation.
8. A DNA sequence encoding a protein of claim 1.
9. A DNA sequence encoding a BMP protein said DNA sequence selected from the group consisting of
 - (a) a DNA sequence encoding BMP-5 comprising the nucleotide #1665 to #2060 of Table III and sequences which hybridize thereto under stringent hybridization conditions and encode a protein characterized by the ability to induce the formation of cartilage and/or bone;
 - (b) a DNA sequence encoding BMP-6 comprising nucleotide #1303 - #1698 of Table IV and sequences which hybridize thereto under stringent hybridization conditions and encode a protein characterized by the ability to induce the formation of cartilage and/or bone;
 - (c) a DNA sequence encoding BMP-7 comprising nucleotide #994 - #1389 of Table V and sequences which hybridize thereto under stringent hybridization conditions and encode a protein characterized by the ability to induce the formation of cartilage and/or bone;
10. A DNA sequence encoding a BMP protein selected from the group consisting of

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- (a) a DNA sequence encoding BMP-5 comprising the nucleotide #669 to #2060 of Table III and sequences which hybridize thereto under stringent hybridization conditions and encode a protein characterized by the ability to induce the formation of cartilage and/or bone;
 - (b) a DNA sequence encoding BMP-6 comprising nucleotide #160 - #1698 of Table IV and sequences which hybridize thereto under stringent hybridization conditions and encode a protein characterized by the ability to induce the formation of cartilage and/or bone;
 - (c) a DNA sequence encoding BMP-7 comprising nucleotide #97 - #1389 of Table V and sequences which hybridize thereto under stringent hybridization conditions and encode a protein characterized by the ability to induce the formation of cartilage and/or bone;
-
- 11. A vector comprising a DNA sequence of claim 8 in operative association with an expression control sequence therefor.
 - 12. A vector comprising a DNA sequence of claim 9 in operative association with an expression control sequence therefor.
 - 13. A vector comprising a DNA sequence of claim 10 in operative association with an expression control sequence therefor.
 - 14. A host cell transformed with a vector of claim

- 11.
15. A host cell transformed with a vector of claim 12.
16. A host cell transformed with a vector of claim 13.
17. A method for producing a purified BMP protein said method comprising the steps of
(a) culturing in a suitable culture medium a transformed host cell of claim 14; and
(b) recovering, isolating and purifying said protein from said culture medium.
18. A method for producing a purified BMP protein said method comprising the steps of
(a) culturing in a suitable culture medium a transformed host cell of claim 15; and
(b) recovering, isolating and purifying said protein from said culture medium.
19. A method for producing a purified BMP protein said method comprising the steps of
(a) culturing in a suitable culture medium a transformed host cell of claim 16; and
(b) recovering, isolating and purifying said protein from said culture medium.
20. A pharmaceutical composition comprising an effective amount of a BMP-5, BMP-6 or BMP-7 protein in admixture with a pharmaceutically acceptable vehicle.
21. A pharmaceutical composition comprising an

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effective amount of a protein of claim 1 in admixture with a pharmaceutically acceptable vehicle.

22. A pharmaceutical composition comprising an effective amount of a protein of claim 2 in admixture with a pharmaceutically acceptable vehicle.
23. A pharmaceutical composition comprising an effective amount of a protein of claim 3 in admixture with a pharmaceutically acceptable vehicle.
24. A composition of claim 20 further comprising a pharmaceutically acceptable matrix.
25. A composition of claim 21 further comprising a pharmaceutically acceptable matrix.
26. A composition of claim 22 further comprising a pharmaceutically acceptable matrix.
27. A composition of claim 23 further comprising a pharmaceutically acceptable matrix.
28. The composition of claim 20 wherein said matrix comprises a material selected from the group consisting of hydroxyapatite, collagen, polylactic acid and tricalcium phosphate.
29. The composition of claim 21 wherein said matrix comprises a material selected from the group consisting of hydroxyapatite, collagen, polylactic acid and tricalcium phosphate.

30. The composition of claim 22 wherein said matrix comprises a material selected from the group consisting of hydroxyapatite, collagen, polylactic acid and tricalcium phosphate.
31. The composition of claim 23 wherein said matrix comprises a material selected from the group consisting of hydroxyapatite, collagen, polylactic acid and tricalcium phosphate.
32. Use of the composition of claim 20 for the treatment of a patient in need of cartilage and/or bone formation.
33. Use of the composition of claim 21 for the treatment of a patient in need of cartilage and/or bone formation.
34. Use of the composition of claim 22 for the treatment of a patient in need of cartilage and/or bone formation.
35. Use of the composition of claim 23 for the treatment of a patient in need of cartilage and/or bone formation.
36. A pharmaceutical composition for wound healing and tissue repair said composition comprising an effective amount of a BMP-5, BMP-6 or BMP-7 protein in a pharmaceutically acceptable vehicle.
37. A pharmaceutical composition for wound healing and tissue repair said composition comprising

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an effective amount of the protein of claim 1 in a pharmaceutically acceptable vehicle.

38. A pharmaceutical composition for wound healing and tissue repair said composition comprising an effective amount of the protein of claim 2 in a pharmaceutically acceptable vehicle.
39. A pharmaceutical composition for wound healing and tissue repair said composition comprising an effective amount of the protein of claim 3 in a pharmaceutically acceptable vehicle.

INTERNATIONAL SEARCH REPORT

International Application No. PCT/US 90/01630

I. CLASSIFICATION OF SUBJECT MATTER (if several classification symbols apply, indicate all)⁵

According to International Patent Classification (IPC) or to both National Classification and IPC

IPC5: C 12 P 21/00, A 61 K 37/36, C 07 K 13/00

II. FIELDS SEARCHED

Minimum Documentation Searched⁶

Classification System:

Classification Symbols

IPC5

C 12 P; A 61 K; C 07 K

Documentation Searched other than Minimum Documentation
to the extent that such Documents are included in Fields Searched⁶

III. DOCUMENTS CONSIDERED TO BE RELEVANT⁹

Category ¹⁰	Citation of Document ¹¹ with indication, where appropriate, of the relevant passages ¹²	Relevant to Claim No. ¹³
A	Proc.Natl.Acad.Sci., Vol. 85, No. 24, 1988, Wang, Elisabeth A et al: "Purification and characterization of other distinct bone-inducing factors", see page 9484 - page 9488	1-39
	--	
A	WO, A1, 8910409 (GENETICS INSTITUTE, INC.) 2 November 1989, see the whole document	1-39
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A	US, A, 4789732 (MARSHALL R. URIST) 6 December 1988, see the whole document	1-39
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Y document of particular relevance, the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

S document member of the same patent family

IV. CERTIFICATION

Date of the Actual Completion of the International Search

20th June 1990

Date of Mailing of this International Search Report

17. 07. 90

International Searching Authority

EUROPEAN PATENT OFFICE

Signature of Authorized Officer

F.W. HECK

III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)

Category *	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No
A	WO, A1, 8800205 (GENETICS INSTITUTE, INC.) 14 January 1988, see the whole document --	1-39
A	EP, A2, 0212474 (UNIVERSITY OF CALIFORNIA) 4 March 1987, see the whole document -- -----	1-39

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